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OM nucleic - nucleic search, using sw model

Run on: September 9, 2004, 13:30:05 ; Search time 23.9144 Seconds
(without alignments)
3730.479 Million cell updates/sec

Title: US-10-082-772B-1

Perfect score: 21

Sequence: 1 ctgctttttataacttg 21

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 337863 seqs, 2124099041 residues

Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N Geneseq_29Jan04:*
1: geneseqn1980s:*
2: geneseqn1990s:*
3: geneseqn2000s:*
4: geneseqn2001as:*
5: geneseqn2001bs:*
6: geneseqn2002s:*
7: geneseqn2003as:*
8: geneseqn2003bs:*
9: geneseqn2003cs:*
10: geneseqn2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	21	100.0	21	2	AAT37370
2	21	100.0	21	4	AAT37370 Bacteriophage
3	21	100.0	21	4	AAT37370 Bacteriophage
4	21	100.0	21	6	ABS76597 Recombina
5	21	100.0	21	7	ACC44645 Nucleotid
6	21	100.0	25	2	AAX78994
7	21	100.0	25	3	AAC55600 Recombina
8	21	100.0	25	4	AAS06276 PCR prime
9	21	100.0	25	4	AAC87897
10	21	100.0	25	4	AAC87896
11	21	100.0	25	4	AAT55765
12	21	100.0	25	4	AAT55766
13	21	100.0	25	8	AAD14459
14	21	100.0	25	8	ACD28426
15	21	100.0	25	8	ACD28427
16	21	100.0	25	8	ACD28605
17	21	100.0	25	8	ACD28606
18	21	100.0	25	8	ADA38193
19	21	100.0	25	8	ADA38192
20	21	100.0	27	9	AAD60588
21	21	100.0	27	4	AAS06174
22	21	100.0	27	7	AAT61422
23	21	100.0	27	7	ABZ58727 Att site
					ACC59571 Nucleic a

24	21	100.0	27	8	ACC85317
25	21	100.0	33	7	ACC44620 Red fluor
26	21	100.0	33	7	ACC44619 Red fluor
27	21	100.0	33	7	ABT16620
28	21	100.0	37	2	AAT37368
29	21	100.0	37	2	AAT37369
30	21	100.0	41	4	AAF61399
31	21	100.0	41	4	AAF61398
32	21	100.0	53	2	AAT64752
33	21	100.0	55	2	AAT64751
34	21	100.0	58	2	AAX78965
35	21	100.0	156	2	AAQ63487
36	21	100.0	386	7	ACA14507
37	21	100.0	2321	3	AAZ51029
38	21	100.0	2337	3	AAZ51030
39	21	100.0	2847	7	ACC44723
40	21	100.0	3166	7	ACC44717
41	21	100.0	3438	7	ACC44695
42	21	100.0	3438	7	ABT16608
43	21	100.0	4223	7	ACC44724
44	21	100.0	4223	7	ACC44714
45	21	100.0	4615	7	ACC44720

ALIGNMENTS

RESULT 1

ID	AAT37370	standard; DNA; 21 BP.
XX	AAT37370;	
AC	AAT37370;	
DT	14-MAY-1997 (first entry)	
XX	Bacteriophage lambda attB site.	
DE	Site-specific recombination; bacterial attachment site; plasmid; vaccine;	
KW	gene therapy; ss.	
XX	Bacteriophage lambda.	
OS	WO9626270-A1.	
PN	29-AUG-1996.	
XX	21-FEB-1996; 96WO-FR000274.	
PF	23-FEB-1995; 95FR-0002117.	
XX	(RHON) RHONE POULENC RORER SA.	
PI	Cameron B, Crouzet J, Darquet A, Scherman D, Wils P;	
XX	WPI; 1996-402363/40.	
DR	Plasmids capable of site-specific recombination - useful for vaccination	
XX	and in gene therapy.	
PT	Claim 17; Page 43; 81pp; French.	
XX	A new expression cassette consists of a gene of interest controlled by a	
CC	promoter and terminator functional in mammalian cells and is flanked by	
CC	sequences in direct orientation which allow site-specific recombination.	
CC	Preferred sequences for site-specific recombination are the bacteriophage	
CC	lambda attP and attB sites. The present sequence is the attB site of	
CC	phage lambda. The expression cassettes can be used for producing plasmids	
CC	which are useful in vaccination or for genetic/ cellular therapy, e.g. of	
CC	dystrophy, cystic fibrosis, Alzheimer's or Parkinson's diseases,	
CC	amyotrophic lateral sclerosis; diseases of	
CC	coagulation/dyslipoproteinaemia or viral infections (AIDS or hepatitis)	
XX	Sequence 21 BP; 4 A; 4 C; 2 G; 11 T; 0 U; 0 Other;	

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Query Match      100.0%; Score 21; DB 2; Length 21;
Best Local Similarity 100.0%; Pred. No. 23;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTGCTTTTATTAATACTTG 21
    |||||
Db 1 CTGCTTTTATTAATACTTG 21

RESULT 2
AAF61417
ID AAF61417 standard; DNA; 21 BP.
XX AC AAF61417;
XX DT 05-JUN-2001 (first entry)
XX DE E. coli attB DNA fragment.
XX KW Sequence-specific recombination; SSR; integrase; gene therapy; somatic;
XX KW targeted integration; attB; ds.
XX OS Escherichia coli.
XX DN DEL9941186-A1.
XX PD 01-MAR-2001.
XX PF 30-AUG-1999; 99DE-01041186.
XX PR 30-AUG-1999; 99DE-01041186.
XX PA (DROE/) DROEGE P.
XX PI Droege P;
XX DR WPI; 2001-246016/26.
XX PT Sequence-specific recombination of DNA in eukaryotes, useful particularly
XX PT for somatic cell gene therapy, uses an integrase to effect recombination
XX PT between att sites.
XX PS Claim 2; Page 13; 24pp; German.
XX CC This invention describes a novel sequence-specific recombination (SSR) of
XX CC DNA in a eukaryotic cell, comprising introducing two DNA sequences (I,
XX CC II) into a cell, using an integrase (Int) to effect SSR. The invention
XX CC also describes (1) a nucleic acid comprising a 243 base pair sequence
XX CC (III), fully defined in the specification, or its derivatives; and (2)
XX CC a vector containing (III), or its derivatives, plus a therapeutic gene, or
XX CC its derivatives. The method is particularly used in somatic gene therapy
XX CC in humans and animals, but can be applied more generally for gene
XX CC transfer to animal or plant cells. The method is simple and controllable,
XX CC and provides stable and targeted integration of selected DNA sequences
XX SQ Sequence 21 BP; 4 A; 4 C; 2 G; 11 T; 0 U; 0 Other;

Query Match      100.0%; Score 21; DB 4; Length 21;
Best Local Similarity 100.0%; Pred. No. 23;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTGCTTTTATTAATACTTG 21
    |||||
Db 1 CTGCTTTTATTAATACTTG 21

RESULT 3
ABS76597
ID ABS76597 standard; DNA; 21 BP.
XX AC ABS76597;
XX DN ABS76597;
XX PF 30-AUG-1999; 99DE-01041186.
XX PR 30-AUG-1999; 99DE-01041186.
XX PA (DROE/) DROEGE P.
XX PI Droege P;
XX DR WPI; 2001-246016/26.
XX PT Sequence-specific recombination of DNA in eukaryotes, useful particularly
XX PT for somatic cell gene therapy, uses an integrase to effect recombination
XX PT between att sites.
XX PS Claim 2; Page 13; 24pp; German.
XX CC This invention describes a novel sequence-specific recombination (SSR) of
XX CC DNA in a eukaryotic cell, comprising introducing two DNA sequences (I,
XX CC II) into a cell, using an integrase (Int) to effect SSR. The invention
XX CC also describes (1) a nucleic acid comprising a 243 base pair sequence
XX CC (III), fully defined in the specification, or its derivatives; and (2)
XX CC a vector containing (III), or its derivatives, plus a therapeutic gene, or
XX CC its derivatives. The method is particularly used in somatic gene therapy
XX CC in humans and animals, but can be applied more generally for gene
XX CC transfer to animal or plant cells. The method is simple and controllable,
XX CC and provides stable and targeted integration of selected DNA sequences
XX SQ Sequence 21 BP; 4 A; 4 C; 2 G; 11 T; 0 U; 0 Other;

Query Match      100.0%; Score 21; DB 4; Length 21;
Best Local Similarity 100.0%; Pred. No. 23;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTGCTTTTATTAATACTTG 21
    |||||
Db 1 CTGCTTTTATTAATACTTG 21

RESULT 4
ACC44645
ID ACC44645 standard; DNA; 21 BP.
XX AC ACC44645;
XX DT 29-MAY-2003 (first entry)
XX DE Nucleotide core region of attB SEQ ID NO:34.
XX KW Chromosome-based platform; artificial chromosome; eukaryotic chromosome;
XX KW att site; integrase; recombinase; ACes; gene therapy; transgenic animal;
XX KW platform artificial chromosome expression system; PCR primer; ss.
XX OS Synthetic.
XX PN WO200297059-A2.
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DT 11-DEC-2002 (first entry)
XX Recombinase recognition site attB.
DE Recombinase recognition site attB.
XX Responder cell; expression construct; screening assay; gene regulation;
XX biosensor; reporter gene construct; recombinase recognition site; ds.
KW Biosensor; reporter gene construct; recombinase recognition site; ds.
XX Synthetic.
OS Synthetic.
XX WO200272789-A2.
PN WO200272789-A2.
XX 19-SEP-2002.
PD 19-SEP-2002.
XX 12-MAR-2002; 2002WO-US008008.
PF 12-MAR-2002; 2002WO-US008008.
XX 12-MAR-2001; 2001US-0274979P.
PR 12-MAR-2001; 2001US-0274979P.
XX 12-MAR-2001; 2001US-0275070P.
PR 12-MAR-2001; 2001US-0275070P.
XX 12-MAR-2001; 2001US-0275148P.
PR 12-MAR-2001; 2001US-0275148P.
XX (IRMI-) IRM LLC.
PA (IRMI-) IRM LLC.
XX Caldwell JS, Su AI, Hogenesch JB;
PI Caldwell JS, Su AI, Hogenesch JB;
XX WPI; 2002-723339/78.
DR WPI; 2002-723339/78.
XX Producing a collection of responder cells for high throughput screening
XX assays, comprises identifying and cloning regulatory regions into
XX expression constructs to control nucleic acids, and introducing into
XX addressable cells.
PS Disclosure; Page 179; 187pp; English.
XX The invention describes producing a collection of responder cells for
XX high throughput screening assays, by identifying and cloning regulatory
XX regions into expression constructs to control nucleic acids, and
XX introducing the constructs into addressable cells. The method is useful
XX in producing cells used in high throughput screening assays for profiling
XX substances and conditions and for studying the function of the regulatory
XX region mediating the response. The cells serve as biosensors to assess
XX the effects of any perturbation, such as external or internal condition,
XX on the cells from which the regulatory regions in the reporter gene
XX constructs are derived can be inferred. This sequence represents a
XX recombinase recognition site that can be incorporated into the expression
XX constructs of the invention
XX SQ Sequence 21 BP; 4 A; 4 C; 2 G; 11 T; 0 U; 0 Other;

Query Match      100.0%; Score 21; DB 6; Length 21;
Best Local Similarity 100.0%; Pred. No. 23;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTGCTTTTATTAATACTTG 21
    |||||
Db 1 CTGCTTTTATTAATACTTG 21

RESULT 4
ACC44645
ID ACC44645 standard; DNA; 21 BP.
XX AC ACC44645;
XX DT 29-MAY-2003 (first entry)
XX DE Nucleotide core region of attB SEQ ID NO:34.
XX KW Chromosome-based platform; artificial chromosome; eukaryotic chromosome;
XX KW att site; integrase; recombinase; ACes; gene therapy; transgenic animal;
XX KW platform artificial chromosome expression system; PCR primer; ss.
XX OS Synthetic.
XX PN WO200297059-A2.
```

XX PD 05-DEC-2002.
 XX PF 30-MAY-2002; 2002WO-US017452.
 XX PR 30-MAY-2001; 2001US-0294758P.
 XX PR 21-MAR-2002; 2002US-0366891P.
 XX PA (CHRO-) CHROMOS MOLECULAR SYSTEMS INC.
 XX PI Perkins E, Perez C, Lindenbaum M, Greene A, Leung J, Fleming E;
 XX PI Stewart S, Shellard J;
 XX DR WPI; 2003-140461/13.
 XX PT Novel eukaryotic chromosome comprising one or many att sites which
 XX PT permits site-directed integration in the presence of lambda-integrase,
 XX PT useful for site-specific recombination-directed integration of DNA of
 XX PT interest.
 XX PS Disclosure; Fig 6; 272pp; English.
 XX CC The present invention describes a eukaryotic chromosome (I) comprising
 XX CC one or several att sites, where an att site is heterologous to the
 XX CC chromosome, and permits site-directed integration in the presence of
 XX CC lambda-integrase. Also described: (1) a platform artificial chromosome
 XX CC expression system (ACes) (II) comprising several sites that participate
 XX CC in recombinase catalysed recombination; and (2) a method (M1) for
 XX CC introducing a heterologous nucleic acid into a platform artificial
 XX CC chromosome. (I) can be used in gene therapy. (M1) is useful for
 XX CC introducing a heterologous nucleic acid molecule into a platform
 XX CC artificial chromosome, preferably an ACes. (II) is useful for producing a
 XX CC transgenic animal (e.g. a fish, insect, reptile, amphibian, arachnid, or
 XX CC mammal) by introducing (II) by cell fusion, lipid-mediated transfection
 XX CC by a carrier system, microinjection, microcell fusion, electroporation,
 XX CC microprojectile bombardment or direct DNA transfer into an embryonic
 XX CC cell, preferably a stem cell or an embryo. (II) comprises a heterologous
 XX CC nucleic acid that encodes a therapeutic product which is useful for
 XX CC making a library of ACes comprising random portions of a genome. ACC44612
 XX CC to ACC44732 and ABP96650 to ABP96657 represent sequences used in the
 XX CC exemplification of the present invention
 XX SQ Sequence 21 BP; 4 A; 4 C; 2 G; 11 T; 0 U; 0 Other;
 Query Match 100.0%; Score 21; DB 7; Length 21;
 Best Local Similarity 100.0%; Pred.No. 23;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CTGCTTTTATCTACTTG 21
 Db 1 CTGCTTTTATCTACTTG 21
 RESULT 5
 AAX78994
 ID AAX78994 standard; DNA; 25 BP.
 XX AC AAX78994;
 XX DT 17-AUG-1999 (first entry)
 XX DE Oligonucleotide #60 for recombination and cloning method.
 XX KW Cloning; donor; recombination site; vector; chimeric; ss.
 XX OS Synthetic.
 XX PN WO9921977-A1.
 XX XX 06-MAY-1999.
 XX PF 26-OCT-1998; 98WO-US022589.
 XX XX

PR 24-OCT-1997; 97US-0065930P.
 PR 23-OCT-1998; 98US-00177387.
 XX PA (LIFE-) LIFE TECHNOLOGIES INC.
 XX PI Hartley JL, Brasch MA, Temple GF, Fox DK;
 XX XX WPI; 1999-303011/25.
 XX DR New nucleic acid cloning methods.
 XX PT Disclosure; Page 176; 185pp; English.
 XX PS
 XX CC The invention relates to novel methods for cloning or subcloning one or
 XX CC more nucleic acid molecules (NAMs) comprising: (a) combining in vitro or
 XX CC in vivo: (1) at least one insert donor molecules (IDMs) comprising one or
 XX CC more desired nucleic acid segments flanked by at least 2 recombination
 XX CC sites which do not recombine with each other; (2) one or more vector
 XX CC donor molecules (VDMs) comprising at least 2 recombination sites which do
 XX CC not recombine with each other; and (3) one or more site-specific
 XX CC recombination proteins; (b) incubating the combination to transfer one or
 XX CC more of the desired segments into one or more of the VDMs, thereby
 XX CC producing one or more desired product molecules (PMs). The methods can be
 XX CC used for the efficient and specific recombination of NAM segments. They
 XX CC can be used to generate chimeric DNA or RNA molecules that have the
 XX CC desired characteristics and/or nucleic acid segments. The methods can
 XX CC also be used for changing vectors. The oligonucleotides AAX78935-X78994
 XX CC are used in the method of the invention
 XX SQ Sequence 25 BP; 6 A; 5 C; 3 G; 11 T; 0 U; 0 Other;
 Query Match 100.0%; Score 21; DB 2; Length 25;
 Best Local Similarity 100.0%; Pred.No. 23;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CTGCTTTTATCTACTTG 21
 Db 4 CTGCTTTTATCTACTTG 24
 RESULT 6
 AAC55600/c
 ID AAC55600 standard; DNA; 25 BP.
 XX AC AAC55600;
 XX DT 11-JAN-2001 (first entry)
 XX DE Recombination efficiency with mutated attB2 site oligonucleotide attB0.
 XX KW Bacteriophage lambda; att; recombination site; attB; attP; attR; attL;
 XX KW mutant; recombinational cloning; entry vector; destination vector;
 XX KW gene product targeting; fusion tag cleavage; PCR primer; ss.
 XX OS Bacteriophage lambda.
 XX OS Synthetic.
 XX PN WO200052027-A1.
 XX XX 08-SEP-2000.
 XX PF 02-MAR-2000; 2000WO-US005432.
 XX XX 02-MAR-1999; 99US-0122389P.
 XX PR 23-MAR-1999; 99US-0126049P.
 XX PR 28-MAY-1999; 99US-0136744P.
 XX XX (LIFE-) LIFE TECHNOLOGIES INC.
 XX PA Hartley JL, Brasch MA, Temple GF, Cheso D;
 XX PI WPI; 2000-543948/49.
 XX DR

PT Isolated nucleic acid molecules encoding an attB1, attB2, attP1, attP2,
 PT attL1, attL2, attR1, and attR2 nucleotide sequence useful for the
 PT recombinational cloning of polypeptides.
 XX
 PS Example 23; Page 157; 459pp; English.
 XX
 CC The present invention describes isolated nucleic acid molecules (I)
 CC encoding an attB1, attB2, attP1, attP2, attL1, attL2, attR1, and attR2
 CC nucleotide sequence. Also described are: (1) an isolated nucleic acid
 CC molecule (II) comprising one or more att recombination sites comprising
 CC at least one mutation in its core region that increases the specificity
 CC of interaction between the recombination site and a second att
 CC recombination site; and (2) an isolated nucleic acid molecule (III)
 CC comprising one or more mutated att recombination sites comprising at
 CC least one mutation in its core region that enhances the efficiency of
 CC recombination between a first nucleic acid molecule comprising the
 CC mutated att recombination site and a second nucleic acid molecule
 CC comprising a second recombination site that interacts with the mutated
 CC att recombination site. (I), (II), (III), primers, vectors and methods
 CC from the present invention are used for the recombinational cloning of
 CC nucleic acid molecules. They can be used for changing vectors, targeting
 CC gene products to intracellular locations, cleaving fusion tags from
 CC desired proteins, operably linking nucleic acid molecules of interest to
 CC regulatory genetic sequences, constructing genes for fusion proteins,
 CC changing copy number, changing replicons, cloning into phages and
 CC cloning. (I), (II), (III), host cells and vectors can be used in the
 CC production of polypeptides and antibodies. The present sequence is used
 CC in the exemplification of the present invention
 XX
 SQ Sequence 25 BP; 11 A; 3 C; 5 G; 6 T; 0 U; 0 Other;

Query Match 100.0%; Score 21; DB 3; Length 25;
 Best Local Similarity 100.0%; Pred. No. 23;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTGCTTTTATATACTACTTG 21
 DB 22 CTGCTTTTATATACTACTTG 2

RESULT 7
 AAS06276/c
 ID AAS06276 standard; DNA; 25 BP.
 AC AAS06276;
 XX
 XX 12-SEP-2001 (first entry)
 DT
 DE PCR primer attB0 used to produce a population of hybrid DNA molecules.
 XX Bacteriophage lambda; recombination; att site; PCR primer; lambda Int;
 KW lambda integrase; therapeutic; ss.
 XX
 XX Bacteriophage lambda.
 OS Synthetic.
 OS
 XX W0200142509-A1.
 PN
 XX 14-JUN-2001.
 PD
 XX 11-DEC-2000; 2000WO-US033546.
 PF
 XX 10-DEC-1999; 99US-0169983P.
 PR 09-MAR-2000; 2000US-0188020P.
 XX
 XX (CHEO/) CHEO D.
 PA (BRAS/) BRASCH M A.
 PA (TEMP/) TEMPLE G F.
 PA (HART/) HARTLEY J L.
 PA (BYRD/) BYRD D R N.
 XX
 XX Chao D, Brasch MA, Temple GF, Hartley JL, Byrd DRN;

DR WPI; 2001-356174/37.

XX Producing hybrid nucleic acids, useful for expressing novel therapeutic
 PT polypeptides, by mixing the same or different nucleic acids having one or
 PT more recombination sites in the presence of recombination proteins, e.g.
 PT Cre.
 PT

XX Example 11; Page 227; 357pp; English.

XX AAS06174-AAS06322 represent Bacteriophage lambda att recombination site
 CC nucleic acid sequences, and PCR primers of the invention. The att
 CC sequences are recognised by the recombination protein lambda integrase
 CC (Int). The invention is a new method of producing a population of hybrid
 CC nucleic acids comprising mixing at least a first population of nucleic
 CC acids comprising one or more recombination sites with at least one target
 CC nucleic acid comprising one or more recombination sites and causing some
 CC or all of the nucleic acids to recombine with all or some of the target
 CC nucleic acids. The method is useful for producing a population of hybrid
 CC nucleic acids which may be the same or different. The nucleic acids may
 CC be used to express therapeutic proteins or peptides and they may also be
 CC used to create novel fusion proteins by expressing different sequences
 CC linked to each other. The method allows simultaneous cloning of two or
 CC more different nucleic acids
 XX
 SQ Sequence 25 BP; 11 A; 3 C; 5 G; 6 T; 0 U; 0 Other;

Query Match 100.0%; Score 21; DB 4; Length 25;
 Best Local Similarity 100.0%; Pred. No. 23;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTGCTTTTATATACTACTTG 21
 DB 22 CTGCTTTTATATACTACTTG 2

RESULT 8
 AAC87897/c
 ID AAC87897 standard; DNA; 25 BP.

AC AAC87897;
 XX
 XX 02-MAR-2001 (first entry)
 DT
 DE Escherichia coli attB oligonucleotide SEQ ID NO:32.
 XX
 XX Core region; recombination site; cloning; chimeric DNA; PCR primer;
 KW characteristic; mutation; att site; lox site; phoA gene; ss.
 XX
 XX Escherichia coli.

XX US6143557-A.
 PN
 XX 07-NOV-2000.
 PD
 XX 20-JAN-1999; 99US-00233493.
 PF
 XX 07-JUN-1995; 95US-00486139.
 PR 07-JUN-1996; 96US-00663002.
 PR 12-JAN-1998; 98US-00005476.
 XX
 XX (LIFE-) LIFE TECHNOLOGIES INC.

XX Brasch MA, Hartley JL;

XX WPI; 2001-049004/06.

XX Isolated nucleic acid molecules comprising a DNA segment having two
 PT engineered recombination sites, derived from att or lox, which flank a
 PT selectable marker and comprise a core region having an engineered
 PT mutation.
 XX

XX Example 3; Col 24; 73pp; English.

XX

CC The present invention describes an isolated nucleic acid molecule (I)
CC comprising a first nucleic acid sequence having a defined sequence
CC (AAC87866 to AAC87881), sequences complementary to AAC87866 to AAC87881,
CC or an RNA sequence corresponding to AAC87866 to AAC87881. Also described
CC are: (1) an isolated nucleic acid molecule (II) comprising a first
CC mutated recombination site that removes one or more stop codons from the
CC recombination site or avoids hairpin formation, the recombination site
CC being an att or lox site; (2) an isolated nucleic acid molecule (III)
CC comprising a first att recombination site comprising a mutation that
CC enhances recombination specificity; (3) vectors (IV) comprising the above
CC mentioned nucleic acids; and (4) cells comprising the above mentioned
CC nucleic acids or (IV). The nucleic acids are used in engineering a core
CC region of a given recombination site to provide mutative sites suitable
CC for subcloning reactions. The use of nucleic acids for obtaining
CC engineered recombination in vitro or in vivo makes the methods for DNA or
CC RNA subcloning, highly specific, rapid, and less labour intensive. The
CC present sequence represents an E. coli attB oligonucleotide, which is
CC used in an example from the present invention
XX
SQ Sequence 25 BP; 11 A; 3 C; 5 G; 6 T; 0 U; 0 Other;

Query Match 100.0%; Score 21; DB 4; Length 25;
Best Local Similarity 100.0%; Pred. No. 23;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTGCTTTTATATACTAACTTG 21
Db 22 CTGCTTTTATATACTAACTTG 2

RESULT 9
AAC87896
ID AAC87896 standard; DNA; 25 BP.
AC AAC87896;
XX
XX 02-WAR-2001 (first entry)
XX
XX Escherichia coli attB oligonucleotide SEQ ID NO:31.
XX
KW Core region; recombination site; cloning; chimeric DNA; PCR primer;
KW characteristic; mutation; att site; lox site; phoA gene; ss.
XX
XX Escherichia coli.
XX
XX US6143557-A.
XX
XX 07-NOV-2000.
XX
XX 20-JAN-1999; 99US-00233493.
XX
XX 07-JUN-1995; 95US-00486139.
XX
XX 07-JUN-1996; 96US-00663002.
XX
XX 12-JAN-1998; 98US-00005476.
XX
XX (LIFE-) LIFE TECHNOLOGIES INC.
XX
XX Brasch MA, Hartley JL;
XX
XX WPI; 2001-049004/06.
XX
XX Isolated nucleic acid molecules comprising a DNA segment having two
XX engineered recombination sites, derived from att or lox, which flank a
XX selectable marker and comprise a core region having an engineered
XX mutation.
XX
XX Example 3; Col 24; 73pp; English.
XX
XX The present invention describes an isolated nucleic acid molecule (I)
XX comprising a first nucleic acid sequence having a defined sequence
XX (AAC87866 to AAC87881), sequences complementary to AAC87866 to AAC87881,
XX or an RNA sequence corresponding to AAC87866 to AAC87881. Also described
XX are: (1) an isolated nucleic acid molecule (II) comprising a first

CC mutated recombination site that removes one or more stop codons from the
CC recombination site or avoids hairpin formation, the recombination site
CC being an att or lox site; (2) an isolated nucleic acid molecule (III)
CC comprising a first att recombination site comprising a mutation that
CC enhances recombination specificity; (3) vectors (IV) comprising the above
CC mentioned nucleic acids; and (4) cells comprising the above mentioned
CC nucleic acids or (IV). The nucleic acids are used in engineering a core
CC region of a given recombination site to provide mutative sites suitable
CC for subcloning reactions. The use of nucleic acids for obtaining
CC engineered recombination in vitro or in vivo makes the methods for DNA or
CC RNA subcloning, highly specific, rapid, and less labour intensive. The
CC present sequence represents an E. coli attB oligonucleotide, which is
CC used in an example from the present invention
XX
SQ Sequence 25 BP; 6 A; 5 C; 3 G; 11 T; 0 U; 0 Other;

Query Match 100.0%; Score 21; DB 4; Length 25;
Best Local Similarity 100.0%; Pred. No. 23;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTGCTTTTATATACTAACTTG 21
Db 4 CTGCTTTTATATACTAACTTG 24

RESULT 10
AAF55765
ID AAF55765 standard; DNA; 25 BP.
XX
XX AAF55765;
XX
XX 12-APR-2001 (first entry)
XX
XX Recombination site attBwt.
XX
XX Recombination site; cloning; att; ss.
XX
XX Unidentified.
XX
XX US6171861-B1.
XX
XX 09-JAN-2001.
XX
XX 12-JAN-1998; 98US-00005476.
XX
XX 07-JUN-1995; 95US-00486139.
XX
XX 07-JUN-1996; 96US-00663002.
XX
XX (LIFE-) LIFE TECHNOLOGIES INC.
XX
XX Hartley JL, Brasch MA;
XX
XX WPI; 2001-136877/14.
XX
XX In vitro cloning of nucleic acid involves mixing vectors comprising
XX recombination sites and/or nucleic acid, incubating mixture to produce
XX chimeric molecule, contacting hosts with mixture and selecting host.
XX
XX Example 3; Col 23; 73pp; English.

XX The present invention relates to a method for in vitro cloning of a
XX nucleic acid of interest. The method involves mixing in vitro two vectors
XX each comprising at least one recombination site and the nucleic acid of
XX interest; incubating the mixture in the presence of at least one
XX recombination protein to result in recombination of the recombination
XX sites, leading to production of a chimeric nucleic acid molecule
XX comprising the nucleic acid of interest; contacting hosts with the
XX mixture; and selecting for a host comprising the chimeric nucleic acid
XX molecule, and selecting against a host comprising the vectors comprising
XX the second vector, to clone the nucleic acid. The present sequence is a
XX recombination site, which may be used in the method of the present
XX invention

```
SQ Sequence 25 BP; 6 A; 5 C; 3 G; 11 T; 0 U; 0 Other;
Query Match 100.0%; Score 21; DB 4; Length 25;
Best Local Similarity 100.0%; Pred. No. 23;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTGCTTTTATATACTAACTTG 21
Db 4 CTGCTTTTATATACTAACTTG 24

RESULT 11
AAF55766/c
ID AAF55766 standard; DNA; 25 BP.
AC AAF55766;
XX
XX 12-APR-2001 (first entry)
XX
XX PCR primer #1.
XX Recombination site; cloning; PCR primer; ss.
XX
XX Unidentified.
XX
XX US6171861-B1.
XX
XX 09-JAN-2001.
XX
XX PF 12-JAN-1998; 98US-00005476.
XX
XX 07-JUN-1995; 95US-00486139.
XX 07-JUN-1996; 96US-00663002.
XX (LIFE-) LIFE TECHNOLOGIES INC.
XX
XX Hartley JL, Brasch MA;
XX WPI; 2001-136877/14.
XX
XX In vitro cloning of nucleic acid involves mixing vectors comprising
XX recombination sites and/or nucleic acid, incubating mixture to produce
XX chimeric molecule, contacting hosts with mixture and selecting host.
XX
XX Disclosure; Col 43-44; 73pp; English.
XX
XX The present invention relates to a method for in vitro cloning of a
XX nucleic acid of interest. The method involves mixing in vitro two vectors
XX each comprising at least one recombination site and the nucleic acid of
XX interest; incubating the mixture in the presence of at least one
XX recombination protein to result in recombination of the recombination
XX sites, leading to production of a chimeric nucleic acid molecule
XX comprising the nucleic acid of interest; contacting hosts with the
XX mixture; and selecting for a host comprising the chimeric nucleic acid
XX molecule, and selecting against a host comprising the vectors comprising
XX the second vector, to clone the nucleic acid. The present sequence is a
XX PCR primer used in the method of the present invention
XX
SQ Sequence 25 BP; 11 A; 3 C; 5 G; 6 T; 0 U; 0 Other;
Query Match 100.0%; Score 21; DB 4; Length 25;
Best Local Similarity 100.0%; Pred. No. 23;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTGCTTTTATATACTAACTTG 21
Db 22 CTGCTTTTATATACTAACTTG 2

RESULT 12
AAD14459
ID AAD14459 standard; DNA; 25 BP.
XX
XX
```

```
AC AAD14459;
XX
XX 01-NOV-2001 (first entry)
XX
XX Recombination site attBwt wild type DNA.
XX
XX Recombination site; copy number; replicon; recombinatorial cloning;
XX attBwt; ds.
XX
XX Unidentified.
XX
XX US6270969-B1.
XX
XX 07-AUG-2001.
XX
XX 20-JAN-1999; 99US-00233492.
XX
XX 07-JUN-1995; 95US-00486139.
XX 07-JUN-1996; 96US-00663002.
XX
XX (INVI-) INVITROGEN CORP.
XX
XX Hartley JL, Brasch MA;
XX WPI; 2001-488248/53.
XX
XX Methods for apposing nucleic acids comprising an expression signal and a
XX gene/partial gene, using recombinatorial cloning by incubating the
XX nucleic acids in the presence of a recombination protein under conditions
XX for recombination.
XX
XX Example 3; Col 23; 76pp; English.
XX
XX The invention relates to a method for apposing an expression signal and a
XX gene or partial gene, using recombinatorial cloning. The method incubates
XX nucleic acids comprising the expression signal and the gene/partial gene
XX in the presence of a recombination protein under conditions sufficient to
XX cause recombination and therefore appose the expression signal and the
XX gene or partial gene. The methods are useful for apposing an expression
XX signal and a gene or partial gene using recombinatorial cloning. The
XX methods are also useful for changing vectors, constructing genes for
XX fusion proteins, changing copy number, changing replicons, cloning into
XX phages, and cloning e.g., PCR products (with an attB site at one end and
XX a loxp site at the other end), genomic DNAs, and cDNAs. The methods are
XX highly specific, rapid, and less labour intensive than prior art methods.
XX The present sequence is a recombination site useful for recombination
XX cloning
XX
SQ Sequence 25 BP; 6 A; 5 C; 3 G; 11 T; 0 U; 0 Other;
Query Match 100.0%; Score 21; DB 4; Length 25;
Best Local Similarity 100.0%; Pred. No. 23;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTGCTTTTATATACTAACTTG 21
Db 4 CTGCTTTTATATACTAACTTG 24

RESULT 13
ACD28426
ID ACD28426 standard; DNA; 25 BP.
XX
XX ACD28426;
XX
XX 02-OCT-2003 (first entry)
XX
XX Wild type attL and attR site recombination sequence attB.
XX
XX Vector donor DNA; ds; flanking recombination site; attB.
XX
XX Synthetic.
XX
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PN US2003064515-A1.
 XX
 PD
 XX 03-APR-2003.
 XX
 PF 30-JAN-2002; 2002US-00058291.
 XX
 PR 07-JUN-1995; 95US-00486139.
 PR 07-JUN-1996; 96US-00663002.
 PR 20-JAN-1999; 99US-00233493.
 PR 02-NOV-1999; 99US-00432085.
 XX
 XX (HART/) HARTLEY J L.
 PA (BRAS/) BRASCH M A.
 XX
 XX Hartley JL, Brasch MA;
 XX
 XX WPI; 2003-540791/51.
 XX
 XX New Vector Donor DNA molecule for recombinational cloning using
 PT engineered recombination sites, comprises first and second DNA segments
 PT that do not recombine with each other and that contain a Selectable
 PT marker.
 XX
 XX Example 3; Page 13; 71pp; English.
 PS
 XX The invention relates to a vector donor DNA molecule comprising a first
 CC DNA segment and a second DNA segment containing at least one selectable
 CC marker. The first and second segments are separated either by, in a
 CC circular vector donor, a first and a second recombination site, or in a
 CC linear vector donor, at least a first recombination site, where each pair
 CC of flanking recombination sites are engineered and do not recombine with
 CC each other. The nucleic acid molecule, vectors and methods are useful for
 CC moving or exchanging segments of DNA molecules using engineered
 CC recombination sites and recombination proteins to provide chimeric DNA
 CC molecules that have the desired characteristic(s) and/or DNA segment(s).
 CC The present sequence represents the wild type attL and attR site
 CC recombination sequence attB
 XX
 XX Sequence 25 BP; 6 A; 5 C; 3 G; 11 T; 0 U; 0 Other;
 SQ
 Query Match 100.0%; Score 21; DB 8; Length 25;
 Best Local Similarity 100.0%; Pred. No. 23;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CTGCTTTTATTAACCTTG 21
 Db 4 CTGCTTTTATTAACCTTG 24
 RESULT 14
 ACD28427/c
 ID ACD28427 standard; DNA; 25 BP.
 XX
 AC ACD28427;
 XX
 DT 02-OCT-2003 (first entry)
 XX
 DE Engineered recombination site associated DNA #1.
 XX
 KW Vector donor DNA; ds; flanking recombination site.
 XX
 XX Synthetic.
 OS
 XX US2003064515-A1.
 PN
 XX 03-APR-2003.
 PD
 XX 30-JAN-2002; 2002US-00058291.
 PF
 XX 07-JUN-1995; 95US-00486139.
 PR 07-JUN-1996; 96US-00663002.
 PR 20-JAN-1999; 99US-00233493.
 PR 02-NOV-1999; 99US-00432085.

XX
 PA (HART/) HARTLEY J L.
 PA (BRAS/) BRASCH M A.
 XX
 XX Hartley JL, Brasch MA;
 XX
 XX WPI; 2003-540791/51.
 XX
 XX New Vector Donor DNA molecule for recombinational cloning using
 PT engineered recombination sites, comprises first and second DNA segments
 PT that do not recombine with each other and that contain a Selectable
 PT marker.
 XX
 XX Disclosure; Page 24; 71pp; English.
 PS
 XX The invention relates to a vector donor DNA molecule comprising a first
 CC DNA segment and a second DNA segment containing at least one selectable
 CC marker. The first and second segments are separated either by, in a
 CC circular vector donor, a first and a second recombination site, or in a
 CC linear vector donor, at least a first recombination site, where each pair
 CC of flanking recombination sites are engineered and do not recombine with
 CC each other. The nucleic acid molecule, vectors and methods are useful for
 CC moving or exchanging segments of DNA molecules using engineered
 CC recombination sites and recombination proteins to provide chimeric DNA
 CC molecules that have the desired characteristic(s) and/or DNA segment(s).
 CC The present sequence represents the engineered recombination site
 CC associated DNA #1
 XX
 XX Sequence 25 BP; 11 A; 3 C; 5 G; 6 T; 0 U; 0 Other;
 SQ
 Query Match 100.0%; Score 21; DB 8; Length 25;
 Best Local Similarity 100.0%; Pred. No. 23;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CTGCTTTTATTAACCTTG 21
 Db 22 CTGCTTTTATTAACCTTG 2
 RESULT 15
 ACD28605
 ID ACD28605 standard; DNA; 25 BP.
 XX
 AC ACD28605;
 XX
 DT 09-OCT-2003 (first entry)
 XX
 DE Wild type attL and attR site recombination sequence attBwt.
 XX
 KW Cointegrate DNA; flanking recombination site; ds; attBwt.
 XX
 OS Synthetic.
 OS
 XX US2003068799-A1.
 PN
 XX 10-APR-2003.
 PD
 XX 06-JUN-2002; 2002US-00162879.
 PF
 XX 07-JUN-1995; 95US-00486139.
 PR 07-JUN-1996; 96US-00663002.
 PR 20-JAN-1999; 99US-00233493.
 PR 02-NOV-1999; 99US-00432085.
 XX
 XX (INVI-) INVITROGEN CORP.
 PA
 XX Hartley JL, Brasch MA;
 PI
 XX WPI; 2003-540884/51.
 DR
 XX Making Cointegrate DNA molecule, by combining recombination sites
 PT flanking the desired DNA segment in insert donor DNA, with the
 PT recombination sites of vector donor DNA, using site specific

```

PT recombination protein.
XX
PS Example 3; Page 14; 7lpp; English.
XX
CC The invention relates to a method of making a cointegrate DNA molecule.
CC The method is useful for making a cointegrate DNA molecule. The method is
CC useful for a variety of DNA exchanges, such as subcloning of DNA, in
CC vitro or in vivo. The method enables efficient and specific recombination
CC of DNA segments using recombination proteins. The method is highly
CC specific, rapid and less labour intensive. The improved specificity,
CC yield and speed of the method facilitates DNA or RNA subcloning,
CC regulation and exchange useful for other related purposes. Since single
CC molecules of the recombinations product can be introduced into a
CC biological host, propagation of the desired product DNA in the absence of
CC other DNA molecules is more readily realised. Reaction conditions can be
CC freely adjusted in vitro to optimise enzyme activities. The present
CC sequence represents the wild type attL and attR site recombination
CC sequence attBwt
XX
SQ Sequence 25 BP; 6 A; 5 C; 3 G; 11 T; 0 U; 0 Other;
Query Match 100.0%; Score 21; DB 8; Length 25;
Best Local Similarity 100.0%; Pred. No. 23;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CTGCTTTTATTAATACTTG 21
Db 4 CTGCTTTTATTAATACTTG 24

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Search completed: September 9, 2004, 18:05:38
Job time : 25.9144 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: September 9, 2004, 19:34:38 ; Search time 26.5292 Seconds
(without alignments)
3982.858 Million cell updates/sec

Title: US-10-082-772B-1

Perfect score: 21
Sequence: 1 ctgctttttataacttg 21

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 3304383 seqs, 2515761380 residues

Total number of hits satisfying chosen parameters: 6608766

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications NA: *

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- 2: /cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq:*
- 3: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*
- 4: /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:*
- 5: /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq:*
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- 11: /cgn2_6/ptodata/2/pubpna/US09C_PUBCOMB.seq:*
- 12: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq:*
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- 19: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	21	100.0	21	10	US-09-981-803-3	Sequence 3, Appli
2	21	100.0	21	15	US-10-252-384-6	Sequence 6, Appli
3	21	100.0	21	15	US-10-161-403-34	Sequence 34, Appli
4	21	100.0	21	17	US-10-097-034A-45	Sequence 45, Appli
5	21	100.0	21	17	US-10-310-695-13	Sequence 13, Appli
6	21	100.0	25	9	US-09-732-914-95	Sequence 95, Appli
7	21	100.0	25	9	US-09-855-797A-60	Sequence 60, Appli
8	21	100.0	25	9	US-09-907-900-60	Sequence 60, Appli
9	21	100.0	25	10	US-09-907-719-60	Sequence 60, Appli
10	21	100.0	25	10	US-09-432-085-31	Sequence 31, Appli
11	21	100.0	25	10	US-09-432-085-32	Sequence 32, Appli
12	21	100.0	25	10	US-09-985-448-60	Sequence 60, Appli
13	21	100.0	25	13	US-10-680-316-60	Sequence 60, Appli
14	21	100.0	25	13	US-10-058-291-31	Sequence 31, Appli

c	15	21	100.0	25	13	US-10-058-291-32	Sequence 32, Appli
c	16	21	100.0	25	15	US-10-058-292-31	Sequence 31, Appli
c	17	21	100.0	25	15	US-10-058-292-32	Sequence 32, Appli
c	18	21	100.0	25	15	US-10-162-879-31	Sequence 31, Appli
c	19	21	100.0	25	15	US-10-162-879-32	Sequence 32, Appli
c	20	21	100.0	25	15	US-10-300-892-60	Sequence 60, Appli
c	21	21	100.0	25	17	US-10-627-711-22	Sequence 22, Appli
c	22	21	100.0	25	17	US-10-815-730-60	Sequence 60, Appli
c	23	21	100.0	25	17	US-10-820-133-60	Sequence 60, Appli
c	24	21	100.0	26	17	US-10-627-711-4	Sequence 4, Appli
c	25	21	100.0	27	9	US-09-732-914-1	Sequence 1, Appli
c	26	21	100.0	27	13	US-10-301-849A-19	Sequence 19, Appli
c	27	21	100.0	27	15	US-10-151-690-25	Sequence 25, Appli
c	28	21	100.0	27	17	US-10-627-711-23	Sequence 23, Appli
c	29	21	100.0	31	13	US-10-403-232-172	Sequence 172, App
c	30	21	100.0	33	15	US-10-161-403-8	Sequence 8, Appli
c	31	21	100.0	33	15	US-10-161-403-9	Sequence 9, Appli
c	32	21	100.0	35	13	US-10-403-232-54	Sequence 54, Appli
c	33	21	100.0	35	13	US-10-403-232-55	Sequence 55, Appli
c	34	21	100.0	37	10	US-09-981-803-1	Sequence 1, Appli
c	35	21	100.0	37	10	US-09-981-803-2	Sequence 2, Appli
c	36	21	100.0	37	15	US-10-252-384-1	Sequence 1, Appli
c	37	21	100.0	37	15	US-10-252-384-2	Sequence 2, Appli
c	38	21	100.0	38	13	US-10-403-232-105	Sequence 105, App
c	39	21	100.0	41	15	US-10-403-232-106	Sequence 106, App
c	40	21	100.0	41	15	US-10-082-772-7	Sequence 7, Appli
c	41	21	100.0	42	13	US-10-082-772-8	Sequence 8, Appli
c	42	21	100.0	42	13	US-10-403-232-73	Sequence 73, Appli
c	43	21	100.0	42	13	US-10-403-232-74	Sequence 74, Appli
c	44	21	100.0	43	10	US-09-981-803-13	Sequence 13, Appli
c	45	21	100.0	45	17	US-10-627-711-11	Sequence 11, Appli

ALIGNMENTS

RESULT 1
US-09-981-803-3
; Sequence 3, Application US/09981803
; Publication No. US20030032092A1
; GENERAL INFORMATION:
; APPLICANT: Joel CROUZET
; APPLICANT: Daniel SCHERMAN
; APPLICANT: Beatrice CAMERON
; APPLICANT: Pierre WILLS
; APPLICANT: Anne-Marie DARQUET
; TITLE OF INVENTION: DNA MOLECULES, PREPARATION AND USE IN GENE THERAPY
; FILE REFERENCE: MINICIRCLE
; CURRENT APPLICATION NUMBER: US/09/981,803
; CURRENT FILING DATE: 2001-10-19
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Description of the artificial sequence:
; OTHER INFORMATION: oligonucleotide
US-09-981-803-3

Query Match 100.0%; Score 21; DB 10; Length 21;
Best Local Similarity 100.0%; Pred. No. 18;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTGCTTTTATATACTACTTG 21

Db 1 CTGCTTTTATATACTACTTG 21

RESULT 2
US-10-252-384-6
; Sequence 6, Application US/10252384

Publication No. US2003010444A1
 GENERAL INFORMATION:
 APPLICANT: CROUZET, Joel
 SCHERMAN, Daniel
 CAMERON, Beatrice
 WILS, Pierre
 DARQUET, Anne-Marie
 TITLE OF INVENTION: DNA MOLECULES, PREPARATION THEREOF AND USE THEREOF IN GENE THERAPY
 NUMBER OF SEQUENCES: 25
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Rhone-Poulenc Rorer Inc.
 STREET: 500 Arcola Road, Mailstop 3c43
 CITY: Collegeville
 STATE: PA
 COUNTRY: USA
 ZIP: 19426
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/10/252,384
 FILING DATE: 24-Sep-2002
 CLASSIFICATION: <Unknown>
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US/08/894,511
 FILING DATE: <Unknown>
 APPLICATION NUMBER: FR 95/02117
 FILING DATE: 23-FEB-1995
 APPLICATION NUMBER: WO 96/00274
 FILING DATE: 21-FEB-1996
 ATTORNEY/AGENT INFORMATION:
 NAME: Savitzky Esq., Martin F.
 REGISTRATION NUMBER: 29,699
 REFERENCE/DOCKET NUMBER: ST95013-US
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (610) 454-3816
 TELEFAX: (610) 454-3808
 INFORMATION FOR SEQ ID NO: 6:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 21 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: double
 TOPOLOGY: linear
 MOLECULE TYPE: other nucleic acid
 DESCRIPTION: /desc = "Oligonucleotide"
 SEQUENCE DESCRIPTION: SEQ ID NO: 6:
 US-10-252-384-6

Query Match 100.0%; Score 21; DB 15; Length 21;
 Best Local Similarity 100.0%; Pred. No. 18;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTGCTTTTATATACTAAGTTG 21
 Db 1 CTGCTTTTATATACTAAGTTG 21

RESULT 3
 US-10-161-403-34
 Sequence 34, Application US/10161403
 Publication No. US20030119104A1
 GENERAL INFORMATION:
 APPLICANT: Perkins, Edward
 APPLICANT: Perez, Carl
 APPLICANT: Lindenbaum, Michael
 APPLICANT: Greene, Amy
 APPLICANT: Leung, Josephine
 APPLICANT: Fleming, Elena
 APPLICANT: Stewart, Sandra
 APPLICANT: Shellard, Joan

TITLE OF INVENTION: CHROMOSOME-BASED PLATFORMS
 FILE REFERENCE: 24601-420
 CURRENT APPLICATION NUMBER: US/10/161,403
 CURRENT FILING DATE: 2002-05-30
 PRIOR APPLICATION NUMBER: 60/294,758
 PRIOR FILING DATE: 2001-05-30
 PRIOR APPLICATION NUMBER: 60/366,891
 PRIOR FILING DATE: 2002-03-21
 NUMBER OF SEQ ID NOS: 129
 SOFTWARE: FastSeq for Windows Version 4.0
 SEQ ID NO 34
 LENGTH: 21
 TYPE: DNA
 ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: attB
 US-10-161-403-34

Query Match 100.0%; Score 21; DB 15; Length 21;
 Best Local Similarity 100.0%; Pred. No. 18;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTGCTTTTATATACTAAGTTG 21
 Db 1 CTGCTTTTATATACTAAGTTG 21

RESULT 4
 US-10-097-034A-45
 Sequence 45, Application US/10097034A
 Publication No. US20040076954A1
 GENERAL INFORMATION:
 APPLICANT: Su, Andrew
 APPLICANT: Hogenesch, John
 APPLICANT: Caldwell, Jeremy
 TITLE OF INVENTION: Genomics-driven High Speed Cellular Assays, Development Thereof
 TITLE OF INVENTION: Collections of Cellular Reporters
 FILE REFERENCE: 38417-1311
 CURRENT APPLICATION NUMBER: US/10/097,034A
 CURRENT FILING DATE: 2002-03-12
 PRIOR APPLICATION NUMBER: 60/275,148
 PRIOR FILING DATE: 2001-03-12
 PRIOR APPLICATION NUMBER: 60/274,979
 PRIOR FILING DATE: 2001-03-12
 PRIOR APPLICATION NUMBER: 60/275,070
 PRIOR FILING DATE: 2001-03-12
 NUMBER OF SEQ ID NOS: 56
 SOFTWARE: FastSeq for Windows Version 4.0
 SEQ ID NO 45
 LENGTH: 21
 TYPE: DNA
 ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: attB
 US-10-097-034A-45

Query Match 100.0%; Score 21; DB 17; Length 21;
 Best Local Similarity 100.0%; Pred. No. 18;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTGCTTTTATATACTAAGTTG 21
 Db 1 CTGCTTTTATATACTAAGTTG 21

RESULT 5
 US-10-310-695-13
 Sequence 13, Application US/10310695
 Publication No. US20040110293A1
 GENERAL INFORMATION:
 APPLICANT: DROGE, PETER
 APPLICANT: ENENKEL, BARBARA
 TITLE OF INVENTION: SEQUENCE SPECIFIC DNA RECOMBINATION IN EUKARYOTIC CELLS

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; FILE REFERENCE: DEBE:019US
; CURRENT APPLICATION NUMBER: US/10/310,695
; CURRENT FILING DATE: 2002-12-05
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 13
; TYPE: DNA
; LENGTH: 21
; ORGANISM: Escherichia coli
US-10-310-695-13
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Query Match 100.0%; Score 21; DB 17; Length 21;
Best Local Similarity 100.0%; Pred. No. 18;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 1 CTGCTTTTATATACTAACTTG 21
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Db 1 CTGCTTTTATATACTAACTTG 21
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RESULT 6

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US-09-732-914-95/c
; Sequence 95, Application US/09732914
; Patent No. US20020007051A1
; GENERAL INFORMATION:
; APPLICANT: Cheo, David
; APPLICANT: Brasch, Michael A.
; APPLICANT: Temple, Gary F.
; APPLICANT: Hartley, James L.
; APPLICANT: Byrd, Devon R.N.
; TITLE OF INVENTION: Use of Multiple Recombination Sites with Unique Specificity in
; TITLE OF INVENTION: Recombinational Cloning
; FILE REFERENCE: 0942.5010002
; CURRENT APPLICATION NUMBER: US/09/732,914
; CURRENT FILING DATE: 2000-12-11
; PRIOR APPLICATION NUMBER: US 60/169,983
; PRIOR FILING DATE: 1999-12-10
; PRIOR APPLICATION NUMBER: US 60/188,020
; PRIOR FILING DATE: 2000-03-09
; NUMBER OF SEQ ID NOS: 140
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 95
; LENGTH: 25
; TYPE: DNA
; ORGANISM: attB0
US-09-732-914-95
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Query Match 100.0%; Score 21; DB 9; Length 25;
Best Local Similarity 100.0%; Pred. No. 19;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 1 CTGCTTTTATATACTAACTTG 21
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Db 22 CTGCTTTTATATACTAACTTG 2
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RESULT 7

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US-09-855-797A-60
; Sequence 60, Application US/09855797A
; Patent No. US20020094574A1
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
; APPLICANT: Temple, Gary F.
; APPLICANT: Fox, Donna K.
; TITLE OF INVENTION: Recombinational Cloning Using Nucleic Acids Having
; TITLE OF INVENTION: Recombination Sites
; FILE REFERENCE: 0942.2850008
; CURRENT APPLICATION NUMBER: US/09/855,797A
; CURRENT FILING DATE: 2001-05-16
; PRIOR APPLICATION NUMBER: 09/296,281
; PRIOR FILING DATE: 1999-04-22
; PRIOR APPLICATION NUMBER: US 60/065,930
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; PRIOR FILING DATE: 1997-10-24
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 60
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: recombination
; OTHER INFORMATION: products
US-09-855-797A-60
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Query Match 100.0%; Score 21; DB 9; Length 25;
Best Local Similarity 100.0%; Pred. No. 19;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 1 CTGCTTTTATATACTAACTTG 21
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Db 4 CTGCTTTTATATACTAACTTG 24
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RESULT 8

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US-09-907-900-60
; Sequence 60, Application US/09907900
; Patent No. US20020172997A1
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
; APPLICANT: Temple, Gary F.
; APPLICANT: Fox, Donna K.
; TITLE OF INVENTION: Recombinational Cloning Using Nucleic Acids Having
; TITLE OF INVENTION: Recombination Sites
; FILE REFERENCE: 0942.2850004
; CURRENT APPLICATION NUMBER: US/09/907,900
; CURRENT FILING DATE: 2001-07-19
; PRIOR APPLICATION NUMBER: 09/177,387
; PRIOR FILING DATE: 1998-10-23
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 60
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: recombination
; OTHER INFORMATION: products
US-09-907-900-60
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Query Match 100.0%; Score 21; DB 9; Length 25;
Best Local Similarity 100.0%; Pred. No. 19;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 1 CTGCTTTTATATACTAACTTG 21
|||
Db 4 CTGCTTTTATATACTAACTTG 24
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RESULT 9

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US-09-907-719-60
; Sequence 60, Application US/09907719
; Publication No. US20020192819A1
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
; APPLICANT: Temple, Gary F.
; APPLICANT: Fox, Donna K.
; TITLE OF INVENTION: Recombinational Cloning Using Nucleic Acids Having
; TITLE OF INVENTION: Recombination Sites
; FILE REFERENCE: 0942.2850004
; CURRENT APPLICATION NUMBER: US/09/907,719
; CURRENT FILING DATE: 2001-07-19
; PRIOR APPLICATION NUMBER: US/09/177,387
; PRIOR FILING DATE: 1998-10-23
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1 NUMBER OF SEQ ID NOS: 60
2 SOFTWARE: PatentIn Ver. 2.0
3 SEQ ID NO 60
4 LENGTH: 25
5 TYPE: DNA
6 ORGANISM: Unknown
7 FEATURE:
8 OTHER INFORMATION: Description of Unknown Organism: recombination
9 OTHER INFORMATION: Products
US-09-907-719-60

Query Match 100.0%; Score 21; DB 9; Length 25;
Best Local Similarity 100.0%; Pred. No. 19;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTGCTTTTATATACTACTTG 21
Db 4 CTGCTTTTATATACTACTTG 24

RESULT 10

US-09-432-085-31
Sequence 31, Application US/09432085
Publication No. US20030100110A1
GENERAL INFORMATION:
APPLICANT: Hartley, James L.
APPLICANT: Brasch, Michael A.
TITLE OF INVENTION: Recombinational Cloning Using Engineered
TITLE OF INVENTION: Recombination Sites
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C
STREET: 1100 New York Ave., N. W. Suite 600
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/432,085
FILING DATE: (Herewith)
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/233,493
FILING DATE: 20-JAN-1999
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/005,476
FILING DATE: 12-JAN-1998
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/663,002
FILING DATE: 07-JUN-1995
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/486,139
FILING DATE: 07-JUN-1995
CLASSIFICATION:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 31:
SEQUENCE CHARACTERISTICS:
LENGTH: 25 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: both
MOLECULE TYPE: cDNA
US-09-432-085-31

Query Match 100.0%; Score 21; DB 10; Length 25;
Best Local Similarity 100.0%; Pred. No. 19;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 CTGCTTTTATATACTACTTG 21
Db 4 CTGCTTTTATATACTACTTG 24

RESULT 11

US-09-432-085-32/c
Sequence 32, Application US/09432085
Publication No. US20030100110A1
GENERAL INFORMATION:
APPLICANT: Hartley, James L.
APPLICANT: Brasch, Michael A.
TITLE OF INVENTION: Recombinational Cloning Using Engineered
TITLE OF INVENTION: Recombination Sites
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C
STREET: 1100 New York Ave., N. W. Suite 600
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/432,085
FILING DATE: (Herewith)
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/233,493
FILING DATE: 20-JAN-1999
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/005,476
FILING DATE: 12-JAN-1998
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/663,002
FILING DATE: 07-JUN-1995
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/486,139
FILING DATE: 07-JUN-1995
CLASSIFICATION:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 32:
SEQUENCE CHARACTERISTICS:
LENGTH: 25 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: both
MOLECULE TYPE: cDNA
US-09-432-085-32

Query Match 100.0%; Score 21; DB 10; Length 25;
Best Local Similarity 100.0%; Pred. No. 19;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTGCTTTTATATACTACTTG 21
Db 22 CTGCTTTTATATACTACTTG 2


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RESULT 12
US-09-985-448-60
; Sequence 60, Application US/09985448
; Publication No. US20030157716A1
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
; APPLICANT: Temple, Gary F.
; APPLICANT: Fox, Donna K.
; TITLE OF INVENTION: Recombinational Cloning Using Nucleic Acids Having
; FILE REFERENCE: 0942.285004
; CURRENT FILING DATE: 2001-11-02
; PRIOR APPLICATION NUMBER: US/09/985,448
; PRIOR FILING DATE: 1998-10-23
; PRIOR APPLICATION NUMBER: US 60/065,930
; PRIOR FILING DATE: 1997-10-24
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 60
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: recombination
; OTHER INFORMATION: products
US-09-985-448-60

Query Match      100.0%; Score 21; DB 10; Length 25;
Best Local Similarity 100.0%; Pred. No. 19;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTGCTTTTATATACTAATTG 21
    |||||
Db 4 CTGCTTTTATATACTAATTG 24

RESULT 13
US-10-680-316-60
; Sequence 60, Application US/10680316
; Publication No. US20040063207A1
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
; APPLICANT: Temple, Gary F.
; APPLICANT: Fox, Donna K.
; TITLE OF INVENTION: Recombinational Cloning Using Nucleic Acids Having
; FILE REFERENCE: 0942.285004
; CURRENT APPLICATION NUMBER: US/10/680,316
; CURRENT FILING DATE: 2003-10-08
; PRIOR APPLICATION NUMBER: US/09/177,387A
; PRIOR FILING DATE: 1998-10-23
; PRIOR APPLICATION NUMBER: US 60/065,930
; PRIOR FILING DATE: 1997-10-24
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 60
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: recombination
; OTHER INFORMATION: products
US-10-680-316-60

Query Match      100.0%; Score 21; DB 13; Length 25;
Best Local Similarity 100.0%; Pred. No. 19;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTGCTTTTATATACTAATTG 21
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Db 4 CTGCTTTTATATACTAATTG 24

RESULT 14
US-10-058-291-31
; Sequence 31, Application US/10058291
; Publication No. US20030064515A1
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
; TITLE OF INVENTION: Recombinational Cloning Using Engineered
; RECOMBINATION SITES
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C
; STREET: 1100 New York Ave., N. W. Suite 600
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/058,291
; FILING DATE: 30-Jan-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/432,085
; FILING DATE: 1999-11-02
; APPLICATION NUMBER: 09/233,493
; FILING DATE: 20-JAN-1999
; APPLICATION NUMBER: 09/005,476
; FILING DATE: 12-JAN-1998
; APPLICATION NUMBER: 08/663,002
; FILING DATE: 07-JUN-1996
; APPLICATION NUMBER: 08/486,139
; FILING DATE: 07-JUN-1995
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 31:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: both
; MOLECULE TYPE: cDNA
; SEQUENCE DESCRIPTION: SEQ ID NO: 31:
US-10-058-291-31

Query Match      100.0%; Score 21; DB 13; Length 25;
Best Local Similarity 100.0%; Pred. No. 19;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTGCTTTTATATACTAATTG 21
    |||||
Db 4 CTGCTTTTATATACTAATTG 24

RESULT 15
US-10-058-291-32/c
; Sequence 32, Application US/10058291
; Publication No. US20030064515A1
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
; TITLE OF INVENTION: Recombinational Cloning Using Engineered
; RECOMBINATION SITES
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:

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ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C
 STREET: 1100 New York Ave., N. W. Suite 600
 CITY: Washington
 STATE: DC
 COUNTRY: USA
 ZIP: 20005-3934
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent In Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/10/058,291
 FILING DATE: 30-Jan-2002
 CLASSIFICATION: <Unknown>
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 09/432,085
 FILING DATE: 1999-11-02
 APPLICATION NUMBER: 09/233,493
 FILING DATE: 20-JAN-1999
 APPLICATION NUMBER: 09/005,476
 FILING DATE: 12-JAN-1998
 APPLICATION NUMBER: 08/663,002
 FILING DATE: 07-JUN-1996
 APPLICATION NUMBER: 08/486,139
 FILING DATE: 07-JUN-1995
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 202-371-2600
 TELEFAX: 202-371-2540
 INFORMATION FOR SEQ ID NO: 32:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 25 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: both
 TOPOLOGY: both
 MOLECULE TYPE: cDNA
 SEQUENCE DESCRIPTION: SEQ ID NO: 32:
 US-10-058-291-32

Query Match 100.0%; Score 21; DB 13; Length 25;
 Best Local Similarity 100.0%; Pred. No. 19;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 CTGCTTTTATTAATACTTG 21
 |||||||
 Db 22 CTGCTTTTATTAATACTTG 2

Search completed: September 10, 2004, 00:14:06
 Job time : 27.5292 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: September 9, 2004, 15:48:15 ; Search time 144.957 Seconds
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Title: US-10-082-772B-1
Perfect score: 21
Sequence: 1 ctgcgtttttataactaacttg 21

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- 9: gb.pr.*
- 10: gb.ro.*
- 11: gb.sts.*
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- 40: em_htgo_mus.*
- 41: em_htgo_other.*

Pred. No. is the number of results predicted by chance to have a

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and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description
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2	21	100.0	21	6	AX092112	AX092112 Sequence
3	21	100.0	25	6	AR124551	AR124551 Sequence
C 4	21	100.0	25	6	AR124552	AR124552 Sequence
5	21	100.0	25	6	AR163202	AR163202 Sequence
C 6	21	100.0	25	6	AR163203	AR163203 Sequence
C 7	21	100.0	25	6	BD263313	BD263313 Compositi
8	21	100.0	25	6	AX491670	AX491670 Sequence
9	21	100.0	25	6	AX498641	AX498641 Sequence
10	21	100.0	25	6	BD131386	BD131386 Recombina
11	21	100.0	26	6	AR142201	AR142201 Sequence
C 12	21	100.0	26	6	AR142202	AR142202 Sequence
13	21	100.0	27	6	A46167	A46167 Sequence 5
C 14	21	100.0	27	6	A46168	A46168 Sequence 6
15	21	100.0	27	6	AR361092	AR361092 Sequence
C 16	21	100.0	27	6	AR361093	AR361093 Sequence
17	21	100.0	27	6	AX787502	AX787502 Sequence
18	21	100.0	37	6	AR265731	AR265731 Sequence
C 19	21	100.0	37	6	AR265732	AR265732 Sequence
C 20	21	100.0	49	6	AR265752	AR265752 Sequence
C 21	21	100.0	53	6	AR142204	AR142204 Sequence
C 22	21	100.0	55	6	AR142203	AR142203 Sequence
23	21	100.0	57	6	AR265753	AR265753 Sequence
24	21	100.0	58	6	BD131357	BD131357 Recombina
25	21	100.0	260	1	ECOLAMATT	J01638 E.coli ATT
C 26	21	100.0	1709	1	ECU39938	U39938 Escherichia
27	21	100.0	2321	6	AR131048	AR131048 Sequence
28	21	100.0	2321	6	BD235468	BD235468 Control o
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30	21	100.0	2321	6	AR350177	AR350177 Sequence
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32	21	100.0	2337	6	BD235469	BD235469 Control o
33	21	100.0	2337	6	AR261941	AR261941 Sequence
34	21	100.0	2337	6	AR350178	AR350178 Sequence
C 35	21	100.0	5872	6	A38246	A38246 Sequence 1
C 36	21	100.0	5872	6	A38251	A38251 Sequence 6
C 37	21	100.0	5872	6	A93674	A93674 Sequence 1
C 38	21	100.0	5872	6	A93679	A93679 Sequence 6
C 39	21	100.0	5872	6	AR101809	AR101809 Sequence
C 40	21	100.0	5872	6	AR101810	AR101810 Sequence
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ALIGNMENTS

RESULT 1
AR265736
LOCUS AR265736 Sequence 6 from patent US 6492164.
DEFINITION AR265736 Sequence 6 from patent US 6492164.
ACCESSION AR265736
VERSION AR265736.1 GI:29694577
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE Unclassified.
1 (bases 1 to 21)
AUTHORS Crouzet,J., Scherman,D., Cameron,B., Wils,P. and Darquet,A.-M.
TITLE Circular DNA expression cassettes for gene transfer
JOURNAL Patent: US 6492164-A 6 10-DEC-2002;
FEATURES Location/Qualifiers

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/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN
Query Match      100.0%; Score 21; DB 6; Length 21;
Best Local Similarity 100.0%; Pred. No. 5.8e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTGCTTTTATACTAATTG 21
    |||||
Db 1 CTGCTTTTATACTAATTG 21

RESULT 2
AX092112
LOCUS      AX092112      21 bp      DNA      linear      PAT 21-MAR-2001
DEFINITION Sequence 1 from Patent WO0116345.
ACCESSION  AX092112
VERSION     AX092112.1 GI:13444355
KEYWORDS   .
ORGANISM   Escherichia coli
SOURCE     Escherichia coli
REFERENCE  1
AUTHORS    Drooge,P.
TITLE      Sequence-specific dna recombination in eukaryotic cells
JOURNAL    Patent: WO 0116345-A 1 08-MAR-2001;
           Drooge, Peter (DE)
FEATURES   Location/Qualifiers
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                        /organism="Escherichia coli"
                        /mol_type="unassigned DNA"
                        /db_xref="taxon:562"

ORIGIN
Query Match      100.0%; Score 21; DB 6; Length 21;
Best Local Similarity 100.0%; Pred. No. 5.8e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTGCTTTTATACTAATTG 21
    |||||
Db 1 CTGCTTTTATACTAATTG 21

RESULT 3
ARI24551
LOCUS      ARI24551      25 bp      DNA      linear      PAT 16-MAY-2001
DEFINITION Sequence 31 from patent US 6171861.
ACCESSION  ARI24551
VERSION     ARI24551.1 GI:14109912
KEYWORDS   .
ORGANISM   Unknown.
SOURCE     Unknown.
REFERENCE  1 (bases 1 to 25)
AUTHORS    Hartley,J.L. and Brasch,M.A.
TITLE      Recombinational cloning using engineered recombination sites
JOURNAL    Patent: US 6171861-A 31 09-JAN-2001;
           Location/Qualifiers
            source          1..25
                        /organism="unknown"
                        /mol_type="unassigned DNA"

ORIGIN
Query Match      100.0%; Score 21; DB 6; Length 25;
Best Local Similarity 100.0%; Pred. No. 5.5e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTGCTTTTATACTAATTG 21
    |||||
Db 4 CTGCTTTTATACTAATTG 24

RESULT 4
ARI24552/c
LOCUS      ARI24552      25 bp      DNA      linear      PAT 16-MAY-2001
DEFINITION Sequence 32 from patent US 6171861.
ACCESSION  ARI24552
VERSION     ARI24552.1 GI:14109913
KEYWORDS   .
ORGANISM   Unknown.
SOURCE     Unknown.
REFERENCE  1 (bases 1 to 25)
AUTHORS    Hartley,J.L. and Brasch,M.A.
TITLE      Recombinational cloning using engineered recombination sites
JOURNAL    Patent: US 6171861-A 32 09-JAN-2001;
           Location/Qualifiers
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Db 22 CTGCTTTTATACTAATTG 2

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DEFINITION Sequence 31 from patent US 6270969.
ACCESSION  ARI63202
VERSION     ARI63202.1 GI:16233722
KEYWORDS   .
ORGANISM   Unknown.
SOURCE     Unknown.
REFERENCE  1 (bases 1 to 25)
AUTHORS    Hartley,J.L. and Brasch,M.A.
TITLE      Recombinational cloning using engineered recombination sites
JOURNAL    Patent: US 6270969-A 31 07-AUG-2001;
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Qy 1 CTGCTTTTATACTAATTG 21
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Db 4 CTGCTTTTATACTAATTG 24

RESULT 6
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DEFINITION Sequence 32 from patent US 6270969.
ACCESSION  ARI63203
VERSION     ARI63203.1 GI:16233725
KEYWORDS   .
ORGANISM   Unknown.
SOURCE     Unknown.
REFERENCE  1 (bases 1 to 25)
AUTHORS    Hartley,J.L. and Brasch,M.A.
TITLE      Recombinational cloning using engineered recombination sites
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JOURNAL Patent: US 6270969-A 32 07-AUG-2001;
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Db 22 CTGCTTTTATATACTAATTG 2
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LOCUS 25 bp DNA linear PAT 17-JUL-2003
DEFINITION Compositions and methods for use in recombinational cloning of
nucleic acids.
ACCESSION BD263313
VERSION BD263313.1 GI:33073081
KEYWORDS JP 2002537790-A/91.
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1 (bases 1 to 25)
AUTHORS Hartley,J.L., Brasch,M.A., Temple,G.F. and Cheo,D.
TITLE Compositions and methods for use in recombinational cloning of
nucleic acids
JOURNAL Patent: JP 2002537790-A 91 12-NOV-2002;
COMMENT INVITROGEN CORP
OS Artificial Sequence
PN JP 2002537790-A/91
PD 12-NOV-2002
PE 02-MAR-2000 JP 2000602252
PR 02-MAR-1999 US 60/122389, 23-MAR-1999 US 60/126049 PR
28-MAY-1999 US 60/136744
PI JAMES L HARTLEY,MICHAEL A BRASCH,GARY F TEMPLE,DAVID CHEO PC
C12N15/09,C07K14/00,C12N1/15,C12N1/19,C12N1/21,C12N5/10,C12N15/ PC
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LOCUS 25 bp DNA linear PAT 16-AUG-2002
DEFINITION Sequence 31 from Patent EP1227147.
ACCESSION AX491670
VERSION AX491670.1 GI:22324178
KEYWORDS .
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1

AUTHORS Hartley,J.L. and Brasch,M.A.
TITLE Recombinational cloning using engineered recombination sites
JOURNAL Patent: EP 1227147-A 31 31-JUL-2002;
INVITROGEN CORPORATION (US)
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Db 4 CTGCTTTTATATACTAATTG 24
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LOCUS 25 bp DNA linear PAT 26-SEP-2002
DEFINITION Sequence 31 from Patent EP1229113.
ACCESSION AX498641
VERSION AX498641.1 GI:23343438
KEYWORDS .
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1
AUTHORS Hartley,J.L. and Brasch,M.A.
TITLE Recombinational cloning using engineered recombination sites
JOURNAL Patent: EP 1229113-A 31 07-AUG-2002;
INVITROGEN CORPORATION (US)
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Db 4 CTGCTTTTATATACTAATTG 24
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LOCUS 25 bp DNA linear PAT 18-SEP-2002
DEFINITION Recombinational cloning using nucleic acids having recombination
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ACCESSION BD131386
VERSION BD131386.1 GI:23226331
KEYWORDS JP 2002500861-A/60.
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1 (bases 1 to 25)
AUTHORS Hartley,J.L., Brasch,M.A., Temple,G.F. and Fox,D.K.
TITLE Recombinational cloning using nucleic acids having recombination
JOURNAL Patent: JP 2002500861-A 60 15-JAN-2002;
LIFE TECHNOLOGIES INC
COMMENT OS Unknown
PN JP 2002500861-A/60
PD 15-JAN-2002
PF 26-OCT-1998 JP 2000518069
PR 24-OCT-1997 US 60/065930, 23-OCT-1998 US 09/177387 PI
JAMES L HARTLEY,MICHAEL A BRASCH,GARY F TEMPLE,DONNA K FOX PC

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C12N15/09,C12O1/68,C12N15/00
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Key source Location/Qualifiers
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DEFINITION Sequence 7 from patent US 6174708.
ACCESSION ARI42201
VERSION ARI42201.1 GI:15102501
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 26)
AUTHORS Sodoyer,R., Aujame,L., Geoffroy,F. and Bouchardon,A.
TITLE Preparation of a multicombinatorial library of antibody gene
expression vectors
JOURNAL Patent: US 6174708-A 7 16-JAN-2001;
FEATURES Location/Qualifiers
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RESULT 12
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DEFINITION Sequence 8 from patent US 6174708.
ACCESSION ARI42202
VERSION ARI42202.1 GI:15102502
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 26)
AUTHORS Sodoyer,R., Aujame,L., Geoffroy,F. and Bouchardon,A.
TITLE Preparation of a multicombinatorial library of antibody gene
expression vectors
JOURNAL Patent: US 6174708-A 8 16-JAN-2001;
FEATURES Location/Qualifiers
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DEFINITION Sequence 5 from Patent WO9521914.
ACCESSION A46167
VERSION A46167.1 GI:2300415
KEYWORDS
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1 (bases 1 to 27)
AUTHORS Sodoyer,R., Aujame,L. and Geoffroy,F.
TITLE METHOD FOR PREPARING A MULTICOMBINATORIAL LIBRARY OF ANTIBODY GENE
EXPRESSION VECTORS
JOURNAL Patent: WO 9521914-A 5 17-AUG-1995;
COMMENT PASTEUR MERIEUX SERUMS VACC (FR)
Other publication AU 1666895 950829
Other publication FR 2715940 950811.
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DEFINITION Sequence 6 from Patent WO9521914.
ACCESSION A46168
VERSION A46168.1 GI:2300416
KEYWORDS
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1 (bases 1 to 27)
AUTHORS Sodoyer,R., Aujame,L. and Geoffroy,F.
TITLE METHOD FOR PREPARING A MULTICOMBINATORIAL LIBRARY OF ANTIBODY GENE
EXPRESSION VECTORS
JOURNAL Patent: WO 9521914-A 6 17-AUG-1995;
COMMENT PASTEUR MERIEUX SERUMS VACC (FR)
Other publication AU 1666895 950829
Other publication FR 2715940 950811.
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ACCESSION AR361092
VERSION   AR361092.1  GI:33768795
KEYWORDS
SOURCE   Unknown.
ORGANISM Unknown.
REFERENCE
1 (bases 1 to 27)
Sodoyer,R., AuJame,L. and Geoffroy,F.
TITLE    Process for preparing a multicombinatorial library of vectors for
expressing antibody genes
JOURNAL  Patent: US 6599697-A 5 29-JUL-2003;
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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

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SUMMARIES

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9	21	100.0	25	3	US-09-296-280-60
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32	21	100.0	2337	4	US-09-562-834-3	Sequence 3, Appli
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35	21	100.0	5872	3	US-08-411-768B-6	Sequence 6, Appli
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37	19.4	92.4	228	4	US-09-107-532A-667	Sequence 667, App
38	19.4	92.4	1407	4	US-09-489-039A-5557	Sequence 5557, App
39	19.4	92.4	2408	1	US-08-486-013-69	Sequence 69, Appl
40	19.4	92.4	2408	2	US-08-482-279-69	Sequence 69, Appl
41	19.4	92.4	2408	2	US-08-342-268-69	Sequence 69, Appl
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43	19.4	92.4	2408	4	US-09-397-386-69	Sequence 69, Appl
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ALIGNMENTS

RESULT 1
US-08-894-511-6
; Sequence 6, Application US/08894511
; Patent No. 6143530
; GENERAL INFORMATION:
; APPLICANT: CROUZET, Joel
; APPLICANT: SCHERMAN, Daniel
; APPLICANT: CAMERON, Beatrice
; APPLICANT: WILDS, Pierre
; APPLICANT: DARQUET, Anne-Marie
; TITLE OF INVENTION: DNA MOLECULES, PREPARATION THEREOF AND
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Rhone-Poulenc Rorer Inc.
; STREET: 500 Arcola Road, Mailstop 3C43
; CITY: Collegeville
; STATE: PA
; COUNTRY: USA
; ZIP: 19426
; COMPUTER READABLE FORM:
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; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
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; FILING DATE:
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: FR 95/02117
; FILING DATE: 23-FEB-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO FR96/00274
; FILING DATE: 21-FEB-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Savitzky Esq., Martin F.
; REGISTRATION NUMBER: 29,699
; REFERENCE/DOCKET NUMBER: ST95013-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (610) 454-3816
; TELEFAX: (610) 454-3808
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 21 base pairs
; TYPE: nucleic acid
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; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
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US-08-894-511-6

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Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 CTGCTTTTATTAACCTTG 21

RESULT 2

US-09-655-728-6
; Sequence 6, Application US/09655728
; Patent No. 6492164
; GENERAL INFORMATION:
; APPLICANT: CROUZET, Joel
; SCHERMAN, Daniel
; CAMERON, Beatrice
; WILS, Pierre
; DARQUET, Anne-Marie
; TITLE OF INVENTION: DNA MOLECULES, PREPARATION THEREOF AND
; USE THEREOF IN GENE THERAPY
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSER: Rhone-Poulenc Rorer Inc.
; STREET: 500 Arcola Road, Mailstop 3C43
; CITY: Collegeville
; STATE: PA
; COUNTRY: USA
; ZIP: 19426

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; MEDIUM TYPE: Floppy disk
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; FILING DATE: 05-Sep-2000
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; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/894,511
; FILING DATE: <Unknown>
; APPLICATION NUMBER: WO FR96/00274
; FILING DATE: 21-FEB-1996

ATTORNEY/AGENT INFORMATION:
; NAME: Savitzky Esq., Martin F.
; REGISTRATION NUMBER: 29,699
; REFERENCE/DOCKET NUMBER: ST95013-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (610) 454-3816
; TELEFAX: (610) 454-3808

INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 21 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
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RESULT 3

US-09-233-493-31

; Sequence 31, Application US/09233493
; Patent No. 6143557
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
; TITLE OF INVENTION: Recombinational Cloning Using Engineered
; TITLE OF INVENTION: Recombination Sites
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSER: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C
; STREET: 1100 New York Ave., N. W. Suite 600
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3934

COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
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; FILING DATE: 20-JAN-1999
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; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/005,476
; FILING DATE: 12-JAN-1998
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/663,002
; FILING DATE: 07-JUN-1996

CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/486,139
; FILING DATE: 07-JUN-1995
; CLASSIFICATION:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 31:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: both
; MOLECULE TYPE: cDNA
US-09-233-493-31

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Best Local Similarity 100.0%; Pred. No. 1.5;
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Db 4 CTGCTTTTATTAACCTTG 24

RESULT 4

US-09-233-493-32/c
; Sequence 32, Application US/09233493
; Patent No. 6143557
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
; TITLE OF INVENTION: Recombinational Cloning Using Engineered
; TITLE OF INVENTION: Recombination Sites
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSER: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C
; STREET: 1100 New York Ave., N. W. Suite 600
; CITY: Washington
; STATE: DC

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; FILING DATE: 07-JUN-1996
; CLASSIFICATION:
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; APPLICATION NUMBER: 08/486,139
; FILING DATE: 07-JUN-1995
; CLASSIFICATION:
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; TELEFAX: 202-371-2540
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; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: both
; MOLECULE TYPE: cdna
; US-09-233-493-32

Query Match 100.0%; Score 21; DB 3; Length 25;
Best Local Similarity 100.0%; Pred. No. 1.5;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTGCTTTTATATACTTG 21
Db 22 CTGCTTTTATATACTTG 2

RESULT 5
US-09-005-476-31
; Sequence 31, Application US/09005476
; Patent No. 6171861
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; TITLE OF INVENTION: Recombinational Cloning Using Engineered
; TITLE OF INVENTION: Recombination Sites
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C.
; STREET: 1100 New York Ave., N. W. Suite 600
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: 08/663,002
; FILING DATE: herewith
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/663,002
; FILING DATE: 07-JUN-1996
; CLASSIFICATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 31:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: both
; MOLECULE TYPE: cdna
; US-09-005-476-31

Query Match 100.0%; Score 21; DB 3; Length 25;
Best Local Similarity 100.0%; Pred. No. 1.5;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTGCTTTTATATACTTG 21
Db 22 CTGCTTTTATATACTTG 2

RESULT 6
US-09-005-476-32/c
; Sequence 32, Application US/09005476
; Patent No. 6171861
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
; TITLE OF INVENTION: Recombinational Cloning Using Engineered
; TITLE OF INVENTION: Recombination Sites
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C.
; STREET: 1100 New York Ave., N. W. Suite 600
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/005,476
; FILING DATE: herewith
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/663,002
; FILING DATE: 07-JUN-1996
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 32:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: both
; MOLECULE TYPE: cdna
; US-09-005-476-32

Query Match 100.0%; Score 21; DB 3; Length 25;
Best Local Similarity 100.0%; Pred. No. 1.5;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTGCTTTTATATACTTG 21
Db 22 CTGCTTTTATATACTTG 2

RESULT 7
US-09-233-492-31
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; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 31:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: both
; MOLECULE TYPE: cdna
; US-09-005-476-31

Query Match 100.0%; Score 21; DB 3; Length 25;
Best Local Similarity 100.0%; Pred. No. 1.5;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTGCTTTTATATACTTG 21
Db 4 CTGCTTTTATATACTTG 24

RESULT 6
US-09-005-476-32/c
; Sequence 32, Application US/09005476
; Patent No. 6171861
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
; TITLE OF INVENTION: Recombinational Cloning Using Engineered
; TITLE OF INVENTION: Recombination Sites
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C.
; STREET: 1100 New York Ave., N. W. Suite 600
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/005,476
; FILING DATE: herewith
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/663,002
; FILING DATE: 07-JUN-1996
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 32:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: both
; MOLECULE TYPE: cdna
; US-09-005-476-32

Query Match 100.0%; Score 21; DB 3; Length 25;
Best Local Similarity 100.0%; Pred. No. 1.5;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTGCTTTTATATACTTG 21
Db 22 CTGCTTTTATATACTTG 2

RESULT 7
US-09-233-492-31
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; Sequence 31, Application US/092333492
; Patent No. 6270969
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
; TITLE OF INVENTION: Recombinational Cloning Using Engineered
; TITLE OF INVENTION: Recombination Sites
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C
; STREET: 1100 New York Ave., N. W. Suite 600
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/233,492
; FILING DATE: 20-JAN-1999
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/663,002
; FILING DATE: 07-JUN-1996
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/486,139
; FILING DATE: 07-JUN-1995
; CLASSIFICATION:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 31:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: both
; MOLECULE TYPE: CDNA
US-09-233-492-31

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Query Match 100.0%; Score 21; DB 3; Length 25;
Best Local Similarity 100.0%; Pred. No. 1.5;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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```

QY 1 CTGCTTTTATATACTAAGTTG 21
Db 4 CTGCTTTTATATACTAAGTTG 24

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RESULT 8
US-09-233-492-32/c
; Sequence 32, Application US/092333492
; Patent No. 6270969
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
; TITLE OF INVENTION: Recombinational Cloning Using Engineered
; TITLE OF INVENTION: Recombination Sites
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C
; STREET: 1100 New York Ave., N. W. Suite 600
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible

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; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/233,492
; FILING DATE: 20-JAN-1999
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/663,002
; FILING DATE: 07-JUN-1996
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/486,139
; FILING DATE: 07-JUN-1995
; CLASSIFICATION:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 32:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: both
; MOLECULE TYPE: CDNA
US-09-233-492-32

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Query Match 100.0%; Score 21; DB 3; Length 25;
Best Local Similarity 100.0%; Pred. No. 1.5;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 CTGCTTTTATATACTAAGTTG 21
Db 22 CTGCTTTTATATACTAAGTTG 2

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RESULT 9
US-09-296-280-60
; Sequence 60, Application US/09296280
; Patent No. 6277608
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
; APPLICANT: Temple, Gary F.
; APPLICANT: Fox, Donna K.
; TITLE OF INVENTION: Recombinational Cloning Using Nucleic Acids Having
; TITLE OF INVENTION: Recombination Sites
; FILE REFERENCE: 0942.2850007
; CURRENT APPLICATION NUMBER: US/09/296,280
; CURRENT FILING DATE: 1999-04-22
; EARLIER APPLICATION NUMBER: US 09/177,387
; EARLIER FILING DATE: 1998-10-23
; EARLIER APPLICATION NUMBER: US 60/065,930
; EARLIER FILING DATE: 1997-10-24
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 60
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: recombination
; OTHER INFORMATION: products
US-09-296-280-60

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Query Match 100.0%; Score 21; DB 3; Length 25;
Best Local Similarity 100.0%; Pred. No. 1.5;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 CTGCTTTTATATACTAAGTTG 21
Db 4 CTGCTTTTATATACTAAGTTG 24

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RESULT 10
US-09-498-074-31
; Sequence 31, Application US/09498074
; Patent No. 6534264
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
; TITLE OF INVENTION: Recombinational Cloning Using Engineered
; TITLE OF INVENTION: Recombination Sites
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C
; STREET: 1100 New York Ave., N. W. Suite 600
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/498,074
; FILING DATE: (Herewith)
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/005,476
; FILING DATE: 12-JAN-1998
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/663,002
; FILING DATE: 07-JUN-1996
; CLASSIFICATION:
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/498,074
; FILING DATE: (Herewith)
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/005,476
; FILING DATE: 12-JAN-1998
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/663,002
; FILING DATE: 07-JUN-1996
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/486,139
; FILING DATE: 07-JUN-1995
; CLASSIFICATION:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2540
; TELEFAX: 202-371-2600
; INFORMATION FOR SEQ ID NO: 31:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: both
; MOLECULE TYPE: cdna
US-09-498-074-31

Query Match 100.0%; Score 21; DB 4; Length 25;
Best Local Similarity 100.0%; Pred. No. 1.5;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTGCTTTTATCTACTG 21
Db 4 CTGCTTTTATCTACTG 24

RESULT 11
US-09-498-074-32/c
; Sequence 32, Application US/09498074
; Patent No. 6534264
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
; TITLE OF INVENTION: Recombinational Cloning Using Engineered
; TITLE OF INVENTION: Recombination Sites
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C
; STREET: 1100 New York Ave., N. W. Suite 600
; CITY: Washington
```

```
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/498,074
; FILING DATE: (Herewith)
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/005,476
; FILING DATE: 12-JAN-1998
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/663,002
; FILING DATE: 07-JUN-1996
; CLASSIFICATION:
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/498,074
; FILING DATE: (Herewith)
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/486,139
; FILING DATE: 07-JUN-1995
; CLASSIFICATION:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 32:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: both
; MOLECULE TYPE: cdna
US-09-498-074-32

Query Match 100.0%; Score 21; DB 4; Length 25;
Best Local Similarity 100.0%; Pred. No. 1.5;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTGCTTTTATCTACTG 21
Db 22 CTGCTTTTATCTACTG 2

RESULT 12
PCT-US96-10082A-31
; Sequence 31, Application PC/TUS9610082A
; GENERAL INFORMATION:
; APPLICANT: Life Technologies, Inc.
; APPLICANT: 8717 Grovemont Circle
; APPLICANT: Gaithersburg, MD 20884-9980
; APPLICANT: United States of America
; APPLICANT: Brasch, Michael A.
; TITLE OF INVENTION: Recombinational Cloning Using Engineered
; TITLE OF INVENTION: Recombination Sites
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C
; STREET: 1100 New York Ave., N. W. Suite 600
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US96/10082A
; FILING DATE: 07-JUN-1996
; CLASSIFICATION:
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; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 31:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: both
; MOLECULE TYPE: cDNA
PCT-US96-10082A-31

Query Match 100.0%; Score 21; DB 5; Length 25;
Best Local Similarity 100.0%; Pred. No. 1.5; Indels 0; Gaps 0;
Matches 21; Conservative 0; Mismatches 0;

QY 1 CTGCTTTTATACAACTTG 21
|||
DB 4 CTGCTTTTATACAACTTG 24

RESULT 13

US-09-101-629A-7
; Sequence 7, Application US/09101629A
; Patent No. 6174708
; GENERAL INFORMATION:
; APPLICANT: Sodoyer, Regis
; APPLICANT: Aujame, Luc
; APPLICANT: Geoffroy, Frederique
; APPLICANT: Bouchardon, Annabelle
; TITLE OF INVENTION: Preparation of a Multicombinatorial Library of Antibody
; FILE REFERENCE: 98,381
; CURRENT APPLICATION NUMBER: US/09/101,629A
; CURRENT FILING DATE: 1999-01-12
; PRIOR APPLICATION NUMBER: PCT/FR96/01938
; PRIOR FILING DATE: 1996-12-04
; PRIOR APPLICATION NUMBER: FR 95 14 325
; PRIOR FILING DATE: 1995-12-04
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 7
; LENGTH: 26
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: AttB Sph+
US-09-101-629A-7

Query Match 100.0%; Score 21; DB 3; Length 26;
Best Local Similarity 100.0%; Pred. No. 1.5; Indels 0; Gaps 0;
Matches 21; Conservative 0; Mismatches 0;

QY 1 CTGCTTTTATACAACTTG 21
|||
DB 2 CTGCTTTTATACAACTTG 22

RESULT 14

US-09-101-629A-8/c
; Sequence 8, Application US/09101629A
; Patent No. 6174708
; GENERAL INFORMATION:
; APPLICANT: Sodoyer, Regis
; APPLICANT: Aujame, Luc
; APPLICANT: Geoffroy, Frederique
; APPLICANT: Bouchardon, Annabelle
; TITLE OF INVENTION: Preparation of a Multicombinatorial Library of Antibody
; FILE REFERENCE: 98,381
; CURRENT APPLICATION NUMBER: US/09/101,629A
; CURRENT FILING DATE: 1999-01-12

; PRIOR APPLICATION NUMBER: PCT/FR96/01938
; PRIOR FILING DATE: 1996-12-04
; PRIOR APPLICATION NUMBER: FR 95 14 325
; PRIOR FILING DATE: 1995-12-04
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 8
; LENGTH: 26
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: AttB Sph-
US-09-101-629A-8

Query Match 100.0%; Score 21; DB 3; Length 26;
Best Local Similarity 100.0%; Pred. No. 1.5; Indels 0; Gaps 0;
Matches 21; Conservative 0; Mismatches 0;

QY 1 CTGCTTTTATACAACTTG 21
|||
DB 21 CTGCTTTTATACAACTTG 1

RESULT 15

US-08-693-234-5
; Sequence 5, Application US/08693234
; Patent No. 6599697
; GENERAL INFORMATION:
; APPLICANT: Sodoyer, ET AL
; TITLE OF INVENTION: PROCESS FOR PREPARING A MULTICOMBINATORIAL LIBRARY OF VECTORS FOR
; FILE REFERENCE: P03144US0/BAS
; CURRENT APPLICATION NUMBER: US/08/693,234
; CURRENT FILING DATE: 1996-10-04
; PRIOR APPLICATION NUMBER: PCT/FR95/00127
; PRIOR FILING DATE: 1995-02-02
; PRIOR APPLICATION NUMBER: FR 94 01519
; PRIOR FILING DATE: 1994-02-10
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
; LENGTH: 27
; TYPE: DNA
; ORGANISM: Escherichia coli
US-08-693-234-5

Query Match 100.0%; Score 21; DB 4; Length 27;
Best Local Similarity 100.0%; Pred. No. 1.5; Indels 0; Gaps 0;
Matches 21; Conservative 0; Mismatches 0;

QY 1 CTGCTTTTATACAACTTG 21
|||
DB 3 CTGCTTTTATACAACTTG 23

Search completed: September 9, 2004, 21:21:16
Job time : 5.63035 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: September 9, 2004, 17:30:16 ; Search time 169.634 Seconds
(without alignments)
3696.811 Million cell updates/sec

Title: US-10-082-772B-1

Perfect score: 21
Sequence: 1 ctgctttttataacttg 21

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 27513289 seqs, 14931090276 residues

Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

EST:*

1: em_estba:*

2: em_esthum:*

3: em_estlin:*

4: em_estmu:*

5: em_estov:*

6: em_estpl:*

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8: em_hcc:*

9: gb_estl:*

10: gb_est2:*

11: gb_hcc:*

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13: gb_est4:*

14: gb_est5:*

15: em_estfun:*

16: em_estom:*

17: em_gss_hum:*

18: em_gss_inv:*

19: em_gss_pln:*

20: em_gss_vrt:*

21: em_gss_fun:*

22: em_gss_mam:*

23: em_gss_mus:*

24: em_gss_pro:*

25: em_gss_rod:*

26: em_gss_phg:*

27: em_gss_vri:*

28: gb_gss1:*

29: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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2	21	100.0	450	28	AQ990483 Rfc01260
3	21	100.0	469	28	AQ990485 Rfc01263
4	21	100.0	517	28	AQ990287 Rfc01035

5	21	100.0	519	28	AQ990174
6	21	100.0	556	28	AQ991338
7	21	100.0	572	28	AQ989502
8	21	100.0	573	28	AQ991578
9	21	100.0	618	28	AQ991068
10	21	100.0	641	28	AQ990513
11	21	100.0	651	28	AQ990758
12	21	100.0	664	28	AQ991011
13	21	100.0	672	28	AQ990864
14	21	100.0	675	28	AQ991241
15	21	100.0	695	28	AQ991039
16	21	100.0	696	28	AQ991211
17	21	100.0	708	28	AQ990869
18	21	100.0	712	28	AQ990809
19	21	100.0	715	28	AQ991358
20	21	100.0	719	28	AQ991352
21	21	100.0	743	28	AQ990346
22	21	100.0	751	28	AQ989566
23	21	100.0	753	28	AQ990861
24	21	100.0	764	28	AQ990110
25	21	100.0	767	28	AQ990301
26	21	100.0	769	28	AQ990470
27	21	100.0	808	28	AQ990388
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29	19.4	92.4	417	12	BM134283
30	19.4	92.4	770	28	AQ991774
31	19.4	92.4	791	28	AQ991791
32	19.4	92.4	829	29	CC546560
33	19.4	92.4	909	13	BX329593
34	19.4	92.4	949	13	BX341052
35	19.4	92.4	962	9	AL526048
36	19.4	92.4	974	13	BX419333
37	19.4	92.4	1014	9	AL536199
38	19.4	92.4	1028	13	BX441494
39	19.4	92.4	1035	13	BX419222
40	19.4	92.4	1035	13	BX459157
41	19.4	92.4	1036	13	BX441486
42	19.4	92.4	1117	13	BX460736
43	19.4	92.4	1119	13	BX362060
44	19.4	92.4	1201	9	AL549604
45	19.4	92.4	1201	13	BX356247

ALIGNMENTS

RESULT 1

AQ990175

LOCUS

DEFINITION

ACCSSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

MEDLINE

PUBMED

COMMENT

AQ990175 427 bp DNA linear GSS 14-AUG-2000
Rfc00900 Phototaxhabdus luminescens strain W14 M13 library
Phototaxhabdus luminescens genomic clone PLG00900, genomic survey
sequence.
AQ990175 1 GI:9648769
GSS
Phototaxhabdus luminescens
Phototaxhabdus luminescens
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Phototaxhabdus.
1 (bases 1 to 427)
ffrench-Constant,R.H., Waterfield,N., Burland,V., Perna,N.T.,
Daborn,P.J., Bowen,D. and Blattner,F.R.
A genomic sample sequence of the entomopathogenic bacterium
Phototaxhabdus luminescens W14: potential implications for virulence
Appl. Environ. Microbiol. 66 (8), 3310-3329 (2000)

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This is one of 2,122 random reads from the M13 library. For
annotation of identified clones (BLASTX, BLASTN and mapping to E.
coli K12 genome) please see french-Constant et al. 2000, Nucleic
Acids Res.
Seq primer: M13 Forward
Class: shotgun.
Location/Qualifiers
1..427
/organism="Photorhabdus luminescens"
/mol_type="genomic DNA"
/strain="W14"
/db_xref="taxon:29488"
/clone="PLG00900"
/dev_stage="primary phase variant"
/clone_lib="Photorhabdus luminescens strain W14 M13
library"
/note="Genomic DNA from strain W14 was size selected (1-2
kb) and then cloned into M13 Janus."

FEATURES
source
Query Match 100.0%; Score 21; DB 28; Length 427;
Best Local Similarity 100.0%; Pred. No. 5.7e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTGCTTTTATATACTAATTG 21
21 CTGCTTTTATATACTAATTG 41

RESULT 2
AQ990483 450 bp DNA linear GSS 14-AUG-2000
LOCUS Rfc01260 Photorhabdus luminescens strain W14 M13 library
DEFINITION Photorhabdus luminescens genomic clone PLG01260, genomic survey
sequence.
ACCESSION AQ990483
VERSION AQ990483.1 GI:9649077
KEYWORDS GSS.
SOURCE Photorhabdus luminescens
ORGANISM Photorhabdus luminescens
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Photorhabdus.
REFERENCE 1 (bases 1 to 450)
AUTHORS french-Constant,R.H., Waterfield,N., Burland,V., Perna,N.T.,
Daborn,P.J., Bowen,D. and Blattner,F.R.
TITLE A genomic sample sequence of the entomopathogenic bacterium
Photorhabdus luminescens W14: potential implications for virulence
JOURNAL Appl. Environ. Microbiol. 66 (8), 3310-3329 (2000)
MEDLINE 20378633
PUBMED 10919786
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coli K12 genome) please see french-Constant et al. 2000, Nucleic
Acids Res.
Seq primer: M13 Forward
Class: shotgun.
Location/Qualifiers
1..450
/organism="Photorhabdus luminescens"
/mol_type="genomic DNA"
/strain="W14"
/db_xref="taxon:29488"
/clone="PLG01260"
/dev_stage="primary phase variant"
/clone_lib="Photorhabdus luminescens strain W14 M13
library"
/note="Genomic DNA from strain W14 was size selected (1-2
kb) and then cloned into M13 Janus."

FEATURES
source
Query Match 100.0%; Score 21; DB 28; Length 450;
Best Local Similarity 100.0%; Pred. No. 5.6e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTGCTTTTATATACTAATTG 21
19 CTGCTTTTATATACTAATTG 39

Db 1 CTGCTTTTATATACTAATTG 21
19 CTGCTTTTATATACTAATTG 39

RESULT 3
AQ990485 469 bp DNA linear GSS 14-AUG-2000
LOCUS Rfc01263 Photorhabdus luminescens strain W14 M13 library
DEFINITION Photorhabdus luminescens genomic clone PLG01263, genomic survey
sequence.
ACCESSION AQ990485
VERSION AQ990485.1 GI:9649079
KEYWORDS GSS.
SOURCE Photorhabdus luminescens
ORGANISM Photorhabdus luminescens
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Photorhabdus.
REFERENCE 1 (bases 1 to 469)
AUTHORS french-Constant,R.H., Waterfield,N., Burland,V., Perna,N.T.,
Daborn,P.J., Bowen,D. and Blattner,F.R.
TITLE A genomic sample sequence of the entomopathogenic bacterium
Photorhabdus luminescens W14: potential implications for virulence
JOURNAL Appl. Environ. Microbiol. 66 (8), 3310-3329 (2000)
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coli K12 genome) please see french-Constant et al. 2000, Nucleic
Acids Res.
Seq primer: M13 Forward
Class: shotgun.
Location/Qualifiers
1..469
/organism="Photorhabdus luminescens"
/mol_type="genomic DNA"
/strain="W14"
/db_xref="taxon:29488"
/clone="PLG01263"
/dev_stage="primary phase variant"
/clone_lib="Photorhabdus luminescens strain W14 M13
library"
/note="Genomic DNA from strain W14 was size selected (1-2
kb) and then cloned into M13 Janus."

FEATURES
source
Query Match 100.0%; Score 21; DB 28; Length 469;
Best Local Similarity 100.0%; Pred. No. 5.5e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTGCTTTTATATACTAATTG 21
27 CTGCTTTTATATACTAATTG 47

Db 1 CTGCTTTTATATACTAATTG 21
27 CTGCTTTTATATACTAATTG 47

RESULT 4
AQ990287

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LOCUS AQ990287 517 bp DNA linear GSS 14-AUG-2000
 DEFINITION RfC01035 Photorhabdus luminescens strain W14 M13 library
 Photorhabdus luminescens genomic clone PLG01035, genomic survey
 sequence.
 ACCESSION AQ990287
 VERSION AQ990287.1 GI:9648881
 KEYWORDS GSS.
 SOURCE Photorhabdus luminescens
 ORGANISM Photorhabdus luminescens
 Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 Enterobacteriaceae; Photorhabdus.
 REFERENCE 1 (bases 1 to 517)
 AUTHORS ffrench-Constant, R.H., Waterfield, N., Burland, V., Perna, N.T.,
 Daborn, P.J., Bowen, D. and Blattner, F.R.
 TITLE A genomic sample sequence of the entomopathogenic bacterium
 Photorhabdus luminescens W14: potential implications for virulence
 JOURNAL Appl. Environ. Microbiol. 66 (8), 3310-3329 (2000)
 MEDLINE 20378633
 PUBMED 10919786
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 coli K12 genome) please see ffrench-Constant et al. 2000, Nucleic
 Acids Res.
 Seq primer: M13 Forward
 Class: shotgun.
 FEATURES
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 Location/Qualifiers
 /organism="Photorhabdus luminescens"
 /mol_type="genomic DNA"
 /strain="W14"
 /db_xref="taxon:29488"
 /clone="PLG01035"
 /dev_stage="primary phase variant"
 /clone_lib="Photorhabdus luminescens strain W14 M13
 library"
 /notes="Genomic DNA from strain W14 was size selected (1-2
 kb) and then cloned into M13 Janus."
 ORIGIN
 Query Match 100.0%; Score 21; DB 28; Length 517;
 Best Local Similarity 100.0%; Pred. No. 5.4e+02;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CTGCTTTTATATACTAATTG 21
 |||
 Db 30 CTGCTTTTATATACTAATTG 50
 |||
 RESULT 5
 AQ990174 519 bp DNA linear GSS 14-AUG-2000
 LOCUS RfC00899 Photorhabdus luminescens strain W14 M13 library
 DEFINITION Photorhabdus luminescens genomic clone PLG00899, genomic survey
 sequence.
 ACCESSION AQ990174
 VERSION AQ990174.1 GI:9648768
 KEYWORDS GSS.
 SOURCE Photorhabdus luminescens
 ORGANISM Photorhabdus luminescens
 Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 Enterobacteriaceae; Photorhabdus.
 REFERENCE 1 (bases 1 to 519)
 AUTHORS ffrench-Constant, R.H., Waterfield, N., Burland, V., Perna, N.T.,
 Daborn, P.J., Bowen, D. and Blattner, F.R.
 TITLE A genomic sample sequence of the entomopathogenic bacterium
 Photorhabdus luminescens W14: potential implications for virulence

JOURNAL Appl. Environ. Microbiol. 66 (8), 3310-3329 (2000)
 MEDLINE 20378633
 PUBMED 10919786
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 annotation of identified clones (BLASTX, BLASTN and mapping to E.
 coli K12 genome) please see ffrench-Constant et al. 2000, Nucleic
 Acids Res.
 Seq primer: M13 Forward
 Class: shotgun.
 FEATURES
 source
 1..519
 Location/Qualifiers
 /organism="Photorhabdus luminescens"
 /mol_type="genomic DNA"
 /strain="W14"
 /db_xref="taxon:29488"
 /clone="PLG00899"
 /dev_stage="primary phase variant"
 /clone_lib="Photorhabdus luminescens strain W14 M13
 library"
 /notes="Genomic DNA from strain W14 was size selected (1-2
 kb) and then cloned into M13 Janus."
 ORIGIN
 Query Match 100.0%; Score 21; DB 28; Length 519;
 Best Local Similarity 100.0%; Pred. No. 5.4e+02;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CTGCTTTTATATACTAATTG 21
 |||
 Db 21 CTGCTTTTATATACTAATTG 41
 |||
 RESULT 6
 AQ991338 556 bp DNA linear GSS 14-AUG-2000
 LOCUS RfC02255 Photorhabdus luminescens strain W14 M13 library
 DEFINITION Photorhabdus luminescens genomic clone PLG02255, genomic survey
 sequence.
 ACCESSION AQ991338
 VERSION AQ991338.1 GI:9649932
 KEYWORDS GSS.
 SOURCE Photorhabdus luminescens
 ORGANISM Photorhabdus luminescens
 Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 Enterobacteriaceae; Photorhabdus.
 REFERENCE 1 (bases 1 to 556)
 AUTHORS ffrench-Constant, R.H., Waterfield, N., Burland, V., Perna, N.T.,
 Daborn, P.J., Bowen, D. and Blattner, F.R.
 TITLE A genomic sample sequence of the entomopathogenic bacterium
 Photorhabdus luminescens W14: potential implications for virulence
 JOURNAL Appl. Environ. Microbiol. 66 (8), 3310-3329 (2000)
 MEDLINE 20378633
 PUBMED 10919786
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 Fax: (44) 1225 826779
 Email: bssrfc@bath.ac.uk
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 annotation of identified clones (BLASTX, BLASTN and mapping to E.
 coli K12 genome) please see ffrench-Constant et al. 2000, Nucleic
 Acids Res.
 Seq primer: M13 Forward
 Class: shotgun.

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FEATURES
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        /dev_stage="primary phase variant"
        /clone_lib="Photorhabdus luminescens strain W14 M13 library"
        /note="Genomic DNA from strain W14 was size selected (1-2 kb) and then cloned into M13 Janus."

ORIGIN
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  Best Local Similarity 100.0%; Pred. No. 5.3e+02;
  Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTGCTTTTATCTACTACTTG 21
Db 20 CTGCTTTTATCTACTACTTG 40

RESULT 7
AQ989502
LOCUS
DEFINITION
  Photorhabdus luminescens strain W14 M13 library
  Rf000051 Photorhabdus luminescens genomic clone PLG00051, genomic survey
  sequence.
ACCESSION
  AQ989502
VERSION
  AQ989502.1 GI:9648096
KEYWORDS
  GSS.
SOURCE
  Photorhabdus luminescens
  Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
  Enterobacteriaceae; Photorhabdus.
REFERENCE
  1 (bases 1 to 572)
  ffrench-Constant,R.H., Waterfield,N., Burland,V., Perna,N.T.,
  Daborn,P.J., Bowen,D. and Blattner,F.R.
  A genomic sample sequence of the entomopathogenic bacterium
  Photorhabdus luminescens W14: potential implications for virulence
  Appl. Environ. Microbiol. 66 (8), 3310-3329 (2000)
20378633
PUBMED
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COMMENT
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  Email: bssr@bath.ac.uk
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  annotation of identified clones (BLASTX, BLASTN and mapping to E.
  coli K12 genome) please see ffrench-Constant et al. 2000, Nucleic
  Acids Res.
  Seq primer: M13 Forward
  Class: shotgun.
  Location/Qualifiers
    1..572
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      /db_xref="taxon:29488"
      /clone="PLG02569"
      /dev_stage="primary phase variant"
      /clone_lib="Photorhabdus luminescens strain W14 M13 library"
      /note="Genomic DNA from strain W14 was size selected (1-2 kb) and then cloned into M13 Janus."

ORIGIN
  Query Match      100.0%; Score 21; DB 28; Length 573;
  Best Local Similarity 100.0%; Pred. No. 5.2e+02;
  Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTGCTTTTATCTACTACTTG 21
Db 31 CTGCTTTTATCTACTACTTG 51

RESULT 8
AQ991578
LOCUS
DEFINITION
  Photorhabdus luminescens strain W14 M13 library
  Rf002569 Photorhabdus luminescens genomic clone PLG02569, genomic survey
  sequence.
ACCESSION
  AQ991578
VERSION
  AQ991578.1 GI:9650172
KEYWORDS
  GSS.
SOURCE
  Photorhabdus luminescens
  Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
  Enterobacteriaceae; Photorhabdus.
REFERENCE
  1 (bases 1 to 573)
  ffrench-Constant,R.H., Waterfield,N., Burland,V., Perna,N.T.,
  Daborn,P.J., Bowen,D. and Blattner,F.R.
  A genomic sample sequence of the entomopathogenic bacterium
  Photorhabdus luminescens W14: potential implications for virulence
  Appl. Environ. Microbiol. 66 (8), 3310-3329 (2000)
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COMMENT
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  Email: bssr@bath.ac.uk
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  annotation of identified clones (BLASTX, BLASTN and mapping to E.
  coli K12 genome) please see ffrench-Constant et al. 2000, Nucleic
  Acids Res.
  Seq primer: M13 Forward
  Class: shotgun.
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      /mol_type="genomic DNA"
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      /dev_stage="primary phase variant"
      /clone_lib="Photorhabdus luminescens strain W14 M13 library"
      /note="Genomic DNA from strain W14 was size selected (1-2 kb) and then cloned into M13 Janus."

ORIGIN
  Query Match      100.0%; Score 21; DB 28; Length 573;
  Best Local Similarity 100.0%; Pred. No. 5.2e+02;
  Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTGCTTTTATCTACTACTTG 21
Db 31 CTGCTTTTATCTACTACTTG 51

RESULT 9
AQ991068
LOCUS
DEFINITION
  Photorhabdus luminescens strain W14 M13 library
  Rf001926 Photorhabdus luminescens genomic clone PLG01926, genomic survey
  sequence.
ACCESSION
  AQ991068
VERSION
  AQ991068.1 GI:9649662
KEYWORDS
  GSS.

```

SOURCE
ORGANISM
Photorhabdus luminescens
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Photorhabdus.

REFERENCE
AUTHORS
ffrench-Constant, R.H., Waterfield, N., Burland, V., Perna, N.T.,
Daborn, P.J., Bowen, D. and Blattner, F.R.

TITLE
A genomic sample sequence of the entomopathogenic bacterium
Photorhabdus luminescens W14: potential implications for virulence

JOURNAL
MEDLINE
20378633
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coli K12 genome) please see fffrench-Constant et al. 2000, Nucleic
Acids Res.

Seq primer: M13 Forward
Class: shotgun.
Location/Qualifiers
1. .618
/organism="Photorhabdus luminescens"
/mol_type="genomic DNA"
/strain="W14"
/db_xref="taxon:29488"
/dev_stage="primary phase variant"
/clone_lib="Photorhabdus luminescens strain W14 M13
library"
/notes="Genomic DNA from strain W14 was size selected (1-2
kb) and then cloned into M13 Janus."

Query Match 100.0%; Score 21; DB 28; Length 618;
Best Local Similarity 100.0%; Pred. No. 5.1e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTGCTTTTATATACTTAACCTG 21
|||||
Db 22 CTGCTTTTATATACTTAACCTG 42

RESULT 10
AQ990513
LOCUS
DEFINITION
Photorhabdus luminescens strain W14 M13 library
sequence.

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Photorhabdus luminescens
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Photorhabdus.

REFERENCE
AUTHORS
ffrench-Constant, R.H., Waterfield, N., Burland, V., Perna, N.T.,
Daborn, P.J., Bowen, D. and Blattner, F.R.

TITLE
A genomic sample sequence of the entomopathogenic bacterium
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coli K12 genome) please see fffrench-Constant et al. 2000, Nucleic
Acids Res.

Seq primer: M13 Forward
Class: shotgun.
Location/Qualifiers
1. .641
/organism="Photorhabdus luminescens"
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/strain="W14"
/db_xref="taxon:29488"
/dev_stage="primary phase variant"
/clone_lib="Photorhabdus luminescens strain W14 M13
library"
/notes="Genomic DNA from strain W14 was size selected (1-2
kb) and then cloned into M13 Janus."

Query Match 100.0%; Score 21; DB 28; Length 641;
Best Local Similarity 100.0%; Pred. No. 5e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTGCTTTTATATACTTAACCTG 21
|||||
Db 26 CTGCTTTTATATACTTAACCTG 46

RESULT 11
AQ990758
LOCUS
DEFINITION
Photorhabdus luminescens strain W14 M13 library
sequence.

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Photorhabdus luminescens
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Photorhabdus.

REFERENCE
AUTHORS
ffrench-Constant, R.H., Waterfield, N., Burland, V., Perna, N.T.,
Daborn, P.J., Bowen, D. and Blattner, F.R.

TITLE
A genomic sample sequence of the entomopathogenic bacterium
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JOURNAL
MEDLINE
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coli K12 genome) please see fffrench-Constant et al. 2000, Nucleic
Acids Res.

Seq primer: M13 Forward
Class: shotgun.
Location/Qualifiers
1. .651
/organism="Photorhabdus luminescens"
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/strain="W14"
/db_xref="taxon:29488"
/clone="PLG01579"

/dev stage="primary phase variant"
/clone_lib="Photorhabdus luminescens strain W14 M13
library"
/note="Genomic DNA from strain W14 was size selected (1-2
kb) and then cloned into M13 Janus."

ORIGIN

Query Match 100.0%; Score 21; DB 28; Length 651;
Best Local Similarity 100.0%; Pred. No. 5e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTGCTTTTATTAAGTACTTG 21
|||||
Db 28 CTGCTTTTATTAAGTACTTG 48

RESULT 12
AQ991011
LOCUS
DEFINITION
Photorhabdus luminescens strain W14 M13 library
Photorhabdus luminescens genomic clone PLG01864, genomic survey
sequence.

ACCESSION AQ991011
VERSION AQ991011.1 GI:9649605

KEYWORDS
SOURCE
ORGANISM
Photorhabdus luminescens

REFERENCE
AUTHORS
1 (bases 1 to 664)
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Photorhabdus.

TITLE
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JOURNAL
MEDLINE
PUBMED
Appl. Environ. Microbiol. 66 (8), 3310-3329 (2000)

COMMENT
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Email: bsrfc@bath.ac.uk
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coli K12 genome) please see ffrrench-Constant et al. 2000, Nucleic
Acids Res.
Seq primer: M13 Forward
Class: shotgun.

FEATURES

source
Location/Qualifiers
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/mol_type="genomic DNA"
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library"
/note="Genomic DNA from strain W14 was size selected (1-2
kb) and then cloned into M13 Janus."

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Query Match 100.0%; Score 21; DB 28; Length 664;
Best Local Similarity 100.0%; Pred. No. 5e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTGCTTTTATTAAGTACTTG 21
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Db 29 CTGCTTTTATTAAGTACTTG 49

RESULT 13
AQ990864
LOCUS
DEFINITION

Photorhabdus luminescens strain W14 M13 library
Photorhabdus luminescens genomic clone PLG01701, genomic survey
sequence.

ACCESSION AQ990864
VERSION AQ990864.1 GI:9649458

KEYWORDS
SOURCE
ORGANISM
Photorhabdus luminescens

Photorhabdus luminescens
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Photorhabdus.

REFERENCE
AUTHORS
1 (bases 1 to 672)
ffrench-Constant, R.H., Waterfield, N., Burland, V., Perna, N.T.,
Daborn, P.J., Bowen, D. and Blattner, F.R.

TITLE
A genomic sample sequence of the entomopathogenic bacterium
Photorhabdus luminescens W14: potential implications for virulence

JOURNAL
MEDLINE
PUBMED
Appl. Environ. Microbiol. 66 (8), 3310-3329 (2000)

COMMENT
Contact: ffrrench-Constant RH
Department of Biology and Biochemistry
University of Bath

South Building, Bath BA2 7AY, UK
Tel: (44) 1225 826621
Fax: (44) 1225 826779

Email: bsrfc@bath.ac.uk
This is one of 2,122 random reads from the M13 library. For
annotation of identified clones (BLASTX, BLASTN and mapping to E.

coli K12 genome) please see ffrrench-Constant et al. 2000, Nucleic
Acids Res.
Seq primer: M13 Forward
Class: shotgun.

FEATURES

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/organism="Photorhabdus luminescens"
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/dev_stage="primary phase variant"
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library"
/note="Genomic DNA from strain W14 was size selected (1-2
kb) and then cloned into M13 Janus."

ORIGIN

Query Match 100.0%; Score 21; DB 28; Length 672;
Best Local Similarity 100.0%; Pred. No. 5e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTGCTTTTATTAAGTACTTG 21
|||||
Db 29 CTGCTTTTATTAAGTACTTG 49

RESULT 14

AQ991241

LOCUS

DEFINITION

Photorhabdus luminescens strain W14 M13 library
Photorhabdus luminescens genomic clone PLG02132, genomic survey
sequence.

ACCESSION AQ991241
VERSION AQ991241.1 GI:9649835

KEYWORDS
SOURCE
ORGANISM
Photorhabdus luminescens

Photorhabdus luminescens
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Photorhabdus.

REFERENCE
AUTHORS
1 (bases 1 to 675)
ffrench-Constant, R.H., Waterfield, N., Burland, V., Perna, N.T.,
Daborn, P.J., Bowen, D. and Blattner, F.R.

TITLE A genomic sample sequence of the entomopathogenic bacterium
JOURNAL Photorhabdus luminescens W14: potential implications for virulence
MEDLINE Appl. Environ. Microbiol. 66 (8), 3310-3329 (2000)
PUBMED 20378633
COMMENT 10919786
Contact: ffrench-Constant RH
Department of Biology and Biochemistry
University of Bath
South Building, Bath BA2 7AY, UK
Tel: (44) 1225 826621
Fax: (44) 1225 826779
Email: bssrfc@bath.ac.uk
This is one of 2,122 random reads from the M13 library. For
annotation of identified clones (BLASTX, BLASTN and mapping to E.
coli K12 genome) please see ffrench-Constant et al. 2000, Nucleic
Acids Res.
Seq primer: M13 Forward
Class: shotgun.
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library"
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kb) and then cloned into M13 Janus."
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Best Local Similarity 100.0%; Pred. No. 5e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 28 CTGCTTTTATTAATACTTG 48
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DEFINITION Photorhabdus luminescens strain W14 M13 library
Photobacterium luminescens genomic clone PLG01894, genomic survey
sequence.
ACCESSION AQ991039.1 GI:9649633
VERSION AQ991039
KEYWORDS GSS.
SOURCE Photorhabdus luminescens
ORGANISM Photorhabdus luminescens
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Photorhabdus.
REFERENCE 1 (bases 1 to 695)
AUTHORS ffrench-Constant,R.H., Waterfield,N., Burland,V., Perna,N.T.,
Daborn,P.J., Bowen,D. and Blattner,F.R.
TITLE A genomic sample sequence of the entomopathogenic bacterium
JOURNAL Photorhabdus luminescens W14: potential implications for virulence
MEDLINE Appl. Environ. Microbiol. 66 (8), 3310-3329 (2000)
PUBMED 20378633
COMMENT 10919786
Contact: ffrench-Constant RH
Department of Biology and Biochemistry
University of Bath
South Building, Bath BA2 7AY, UK
Tel: (44) 1225 826621
Fax: (44) 1225 826779
Email: bssrfc@bath.ac.uk
This is one of 2,122 random reads from the M13 library. For
annotation of identified clones (BLASTX, BLASTN and mapping to E.
coli K12 genome) please see ffrench-Constant et al. 2000, Nucleic
Acids Res.

Seq primer: M13 Forward
Class: shotgun.
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library"
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kb) and then cloned into M13 Janus."
ORIGIN
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Best Local Similarity 100.0%; Pred. No. 4.9e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CTGCTTTTATTAATACTTG 21
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Db 30 CTGCTTTTATTAATACTTG 50
|||
Search completed: September 9, 2004, 21:18:21
Job time : 171.634 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: September 9, 2004, 17:33:11 ; Search time 53.5798 Seconds
(without alignments)
2516.866 Million cell updates/sec

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Perfect score: 243
Sequence: 1 tctgttacaggctcactaata.....taaaatcattattgatttc 243

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 682709 seqs, 277475446 residues

Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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C 2	243	100.0	6043	4	US-09-630-929-4
C 3	243	100.0	7652	1	US-07-590-988A-1
4	144	59.3	201	1	US-08-021-667A-18
5	144	59.3	201	1	US-08-410-544-18
6	144	59.3	201	1	US-08-728-785A-18
7	104.6	43.0	38584	4	US-09-453-702B-50
8	100.4	41.3	2408	1	US-08-486-013-69
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13	100.4	41.3	3484	4	US-09-308-090-1
14	100.4	41.3	3484	4	US-09-380-090A-1
15	100.4	41.3	3757	2	US-09-016-366A-13
16	100.4	41.3	3757	2	US-08-978-404B-19
C 17	100.4	41.3	5349	4	US-09-068-101-7
C 18	100.4	41.3	5611	4	US-09-068-101-10
19	97.4	40.1	200	1	US-08-021-667A-17
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21	97.4	40.1	200	1	US-08-728-785A-17
C 22	96	39.5	9827	4	US-09-453-702B-66
23	78.6	32.3	228	4	US-09-107-532A-667
24	45.8	18.8	640681	4	US-09-790-988-1
25	44.6	18.4	7786	4	US-09-790-988-2
26	41.6	17.1	10467	4	US-10-204-708-2
27	41	16.9	3078	4	US-09-601-198-54

C 28	40	16.5	408	4	US-09-621-976-8544	Sequence 8544, Ap
C 29	40	16.5	4185	4	US-09-417-485D-7	Sequence 7, Appli
C 30	39.6	16.3	732	4	US-09-134-000C-2779	Sequence 2779, Ap
31	39.6	16.3	6866	4	US-10-204-708-19	Sequence 19, Appl
32	39.2	16.1	3680	4	US-09-647-390-15	Sequence 15, Appl
33	39.2	16.1	6768	1	US-08-107-755A-1	Sequence 1, Appli
34	39.2	16.1	8457	1	US-07-991-867B-1	Sequence 1, Appli
35	39.2	16.1	8457	2	US-08-544-332-1	Sequence 1, Appli
36	39.2	16.1	8457	4	US-09-370-861A-1	Sequence 13, Appl
C 37	39.2	16.1	19124	2	US-08-487-826B-13	Sequence 33, Appl
C 38	39	16.0	1117	3	US-09-247-373B-33	Sequence 3, Appli
39	39	16.0	10619	4	US-10-204-708-3	Sequence 38, Appl
C 40	38.8	16.0	1048	4	US-09-489-847-38	Sequence 39, Appl
41	38.8	16.0	19513	4	US-10-204-708-39	Sequence 3, Appli
42	38.6	15.9	1151	1	US-08-236-754-3	Sequence 1, Appli
43	38.6	15.9	3055	1	US-08-236-754-1	Patent No. 5231168
C 44	38.6	15.9	3095	6	5231168-1	Sequence 89, Appl
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ALIGNMENTS

RESULT 1
US-08-556-978B-78/c
; Sequence 78, Application US/08556978B
; Patent No. 6268169
; GENERAL INFORMATION:
; APPLICANT: FAHNESTOCK, STEPHEN F.
; TITLE OF INVENTION: NOVEL RECOMBINANTLY PRODUCED
; TITLE OF INVENTION: SPIDER SILK ANALOGS
; NUMBER OF SEQUENCES: 107
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: E. I. DU PONT DE NEMOURS AND COMPANY
; STREET: 1007 MARKET STREET
; CITY: WILMINGTON
; STATE: DELAWARE
; COUNTRY: UNITED STATES OF AMERICA
; ZIP: 19898
; COMPUTER READABLE FORM:
; MEDIUM TYPE: DISKETTE, 3.50 INCH
; COMPUTER: IBM PC COMPATIBLE
; OPERATING SYSTEM: MICROSOFT WINDOWS 95
; SOFTWARE: MICROSOFT WORD FOR WINDOWS 95
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/556,978B
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/077,600
; FILING DATE: JUNE 15, 1993
; ATTORNEY/AGENT INFORMATION:
; NAME: FLOYD, LINDA AXAMETHY
; REGISTRATION NUMBER: 33,692
; REFERENCE/DOCKET NUMBER: CR-9389-A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 302-892-8112
; TELEFAX: 302-773-0164
; INFORMATION FOR SEQ ID NO: 78:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4909 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: circular
; MOLECULE TYPE: DNA (genomic)
US-08-556-978B-78

Query Match 100.0%; Score 243; DB 3; Length 4909;
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Db 2516 TCTGTTACAGGTCACCTAATACCATCTAAGTAGTGTGATTCATAGTGCATATGTTGTG 2457
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Db 2456 TTTTACAGTATTATGATGCTGCTTTTATGCAAAATCTAAATTAATATATGATATTTA 2397
QY 121 TATCATTTTACGTTTCTCGTTCAGCTTTTATATCTAAGTTCGCAATATAAAAAAGCATT 180
Db 2396 TATCATTTTACGTTTCTCGTTCAGCTTTTATATCTAAGTTCGCAATATAAAAAAGCATT 2337
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Db 2336 GCTTATCAATTTGTTGCAACGAGTCACATCATCATGTCAGTCAAAATATAATCAATTTTAT 2277
QY 241 TTC 243
Db 2276 TTC 2274

RESULT 2

US-09-630-929-4/c
; Sequence 4, Application US/09630929
; Patent No. 6620585
; GENERAL INFORMATION:
; APPLICANT: Judith W. Zyskind
; TITLE OF INVENTION: USE OF ECTOENZYMES AND SECRETED ENZYMES
; FILE REFERENCE: ELTRA.012A
; CURRENT APPLICATION NUMBER: US/09/630,929
; CURRENT FILING DATE: 2000-08-02
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 6043
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Engineered E. coli plasmid pJFK4 with V. harveyi
; OTHER INFORMATION: sequences inserted
US-09-630-929-4

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Best Local Similarity 100.0%; Pred. No. 9.9e-45;
Matches 243; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 61 TTTTACAGTATTATGATGCTGCTTTTATGCAAAATCTAAATTAATATATGATATTTA 120
Db 5354 TTTTACAGTATTATGATGCTGCTTTTATGCAAAATCTAAATTAATATATGATATTTA 5295
QY 121 TATCATTTTACGTTTCTCGTTCAGCTTTTATATCTAAGTTCGCAATATAAAAAAGCATT 180
Db 5294 TATCATTTTACGTTTCTCGTTCAGCTTTTATATCTAAGTTCGCAATATAAAAAAGCATT 5235
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Db 5234 GCTTATCAATTTGTTGCAACGAGTCACATCATCATGTCAGTCAAAATATAATCAATTTTAT 5175
QY 241 TTC 243
Db 5174 TTC 5172

RESULT 3

US-07-590-988A-1
; Sequence 1, Application US/07590988A
; Patent No. 5227288
; GENERAL INFORMATION:
; APPLICANT: Blattner, Frederick R.
; TITLE OF INVENTION: DNA Sequencing Vector with

; TITLE OF INVENTION: Reversible Insert
; NUMBER OF SEQUENCES: 1
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Quarles and Brady
; STREET: P.O BOX 2113
; CITY: MADISON
; STATE: WISCONSIN
; COUNTRY: U.S.A.
; ZIP: 53701
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette - 3.50 inch, 800Kb storage
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Macintosh
; SOFTWARE: Microsoft Word 4.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/590,988A
; FILING DATE: 19901001
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Nicholas J. Seay
; REGISTRATION NUMBER: 27,386
; REFERENCE/DOCKET NUMBER: 9629691682
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (608) 251-5000
; TELEFAX: (608) 251-9166
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7652 base pairs
; TYPE: NUCLEIC ACID
; STRANDEDNESS: double
; TOPOLOGY: circular
; MOLSCULE TYPE: Other nucleic acid;
; DESCRIPTION: synthetic recombinant plasmid
; HYPOTHETICAL: no
; ANTI-SENSE: no
US-07-590-988A-1

Query Match 100.0%; Score 243; DB 1; Length 7652;
Best Local Similarity 100.0%; Pred. No. 1e-44;
Matches 243; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 5993 TTTTACAGTATTATGATGCTGCTTTTATGCAAAATCTAAATTAATATATGATATTTA 6052
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Db 6173 TTC 6175

RESULT 4

US-08-021-667A-18
; Sequence 18, Application US/08021667A
; Patent No. 5434049
; GENERAL INFORMATION:
; APPLICANT: Okano, Kazunori
; APPLICANT: Kambara, Hideki
; TITLE OF INVENTION: POLYNUCLEOTIDE CAPTURING TIP AND
; TITLE OF INVENTION: POLYNUCLEOTIDE PREPARATIVE METHOD AND DETECTION
; TITLE OF INVENTION: METHOD USING SAME


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;
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Antonelli, Terry, Stout & Kraus
; STREET: Suite 600, 1919 Pennsylvania Ave., NW
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20006
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/021,667A
; FILING DATE: 19930224
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Terry, David T.
; REGISTRATION NUMBER: 20,178
; REFERENCE/DOCKET NUMBER: 520.31930X00
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-828-0300
; TELEFAX: 202-828-0380
; TELEX: 440280/248545
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 201 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: YES
; ANTI-SENSE: NO
; US-08-021-667A-18

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Matches 144; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 160 TTGGCATTATAAAAGCATTGCTTATCATTTTGTGCAACGACAGGTCACTATCAGTC 219
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QY 220 AAAATAAAATCAATTATTGATTTTC 243
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RESULT 5
US-08-410-544-18
; Sequence 18, Application US/08410544
; Patent No. 5607646
; GENERAL INFORMATION:
; APPLICANT: Okano, Kazunori
; APPLICANT: Kambara, Hideki
; TITLE OF INVENTION: POLYNUCLEOTIDE CAPTURING TIP AND
; TITLE OF INVENTION: POLYNUCLEOTIDE PREPARATIVE METHOD AND DETECTION
; TITLE OF INVENTION: METHOD USING SAME
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Antonelli, Terry, Stout & Kraus
; STREET: Suite 600, 1919 Pennsylvania Ave., NW
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20006
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
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; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/410,544
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/021,667
; FILING DATE: 24-FEB-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Terry, David T.
; REGISTRATION NUMBER: 20,178
; REFERENCE/DOCKET NUMBER: 520.31930X00
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-828-0300
; TELEFAX: 202-828-0380
; TELEX: 248545
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 201 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: YES
; ANTI-SENSE: NO
; US-08-410-544-18

Query Match 59.3%; Score 144; DB 1; Length 201;
Best Local Similarity 100.0%; Pred. No. 2.6e-23;
Matches 144; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 100 AATTTAATATATTGATATTTATATCATTTTACGGTTCTCGTTACGCTTTTCTGTTTATACCTAAG 159
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QY 160 TTGGCATTATAAAAGCATTGCTTATCATTTTGTGCAACGACAGGTCACTATCAGTC 219
Db 61 TTGGCATTATAAAAGCATTGCTTATCATTTTGTGCAACGACAGGTCACTATCAGTC 120
QY 220 AAAATAAAATCAATTATTGATTTTC 243
Db 121 AAAATAAAATCAATTATTGATTTTC 144

RESULT 6
US-08-728-785A-18
; Sequence 18, Application US/08728785A
; Patent No. 5817506
; GENERAL INFORMATION:
; APPLICANT: Okano, Kazunori
; APPLICANT: Kambara, Hideki
; TITLE OF INVENTION: POLYNUCLEOTIDE CAPTURING TIP AND
; TITLE OF INVENTION: POLYNUCLEOTIDE PREPARATIVE METHOD AND DETECTION
; TITLE OF INVENTION: METHOD USING SAME
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Antonelli, Terry, Stout & Kraus
; STREET: Suite 1800, 1300 No. 5817506th Seventeenth St.
; CITY: Arlington
; STATE: VA
; COUNTRY: USA
; ZIP: 22209
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/728,785A
; FILING DATE: 10-OCT-1996
; CLASSIFICATION: 435
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RESULT 7
US-09-453-702B-50
Sequence 50, Application US/09453702B
Patent No. 6365723
GENERAL INFORMATION:
APPLICANT: Blattner, Frederick R.
Burland, Valerie
Perna, Nicole I.
Plunkett, Guy
Welch, Rod
TITLE OF INVENTION: No. 6365723el Sequences of E. coli 0157
NUMBER OF SEQUENCES: 265
CORRESPONDENCE ADDRESS:
ADDRESSEE: Quarles & Brady
STREET: 1 South Pinckney Street
CITY: Madison
STATE: WI
COUNTRY: US
ZIP: 53701-2113
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch. 1.44Mb storage
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect 8.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/453,702B
FILING DATE: 03-Dec-1999
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/110,955
FILING DATE: 04-DEC-1998
ATTORNEY/AGENT INFORMATION:

RESULT 8

TELEFAX: (619) 535-8949
 INFORMATION FOR SEQ ID NO: 69:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 2408 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 US-08-486-013-69

Query Match 41.3%; Score 100.4; DB 1; Length 2408;
 Best Local Similarity 99.0%; Pred. No. 9.6e-14;
 Matches 101; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 142 CAGCTTTTATCTAAGTTGGCATTATATAAAAGCATTGCTTATCAATTTGTTGCAACG 201
 DB 408 CTGCTTTTATCTAAGTTGGCATTATATAAAAGCATTGCTTATCAATTTGTTGCAACG 467
 QY 202 AACAGGTCACATCAGTCAAAATAAAATCAATTTGATTTC 243
 DB 468 AACAGGTCACATCAGTCAAAATAAAATCAATTTGATTTC 509

RESULT 9
 US-08-482-279-69
 ; Sequence 69, Application US/08482279
 ; Patent No. 5840498
 ; GENERAL INFORMATION:
 ; APPLICANT: Selsted, Michael E.
 ; APPLICANT: Ouellette, Andre J.
 ; TITLE OF INVENTION: Antibiotic Cryptdin Peptides and Methods
 ; TITLE OF INVENTION: of their Use
 ; NUMBER OF SEQUENCES: 70
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Campbell and Flores
 ; STREET: 4370 La Jolla Village Drive, Suite 700
 ; CITY: San Diego
 ; STATE: California
 ; COUNTRY: USA
 ; ZIP: 92122
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patentin Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/482,279
 ; FILING DATE:
 ; CLASSIFICATION: 530
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/342,268
 ; FILING DATE: 18-NOV-1994
 ; APPLICATION NUMBER: US 07/930,649
 ; FILING DATE: 14-AUG-1992
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 07/889,020
 ; FILING DATE: 26-MAY-1992
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Campbell, Cathryn A.
 ; REGISTRATION NUMBER: 31,815
 ; REFERENCE/DOCKET NUMBER: P-UC 1206
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (619) 535-8949
 ; TELEFAX: (619) 535-8949
 ; INFORMATION FOR SEQ ID NO: 69:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 2408 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 US-08-482-279-69

Query Match 41.3%; Score 100.4; DB 2; Length 2408;
 Best Local Similarity 99.0%; Pred. No. 9.6e-14;

Matches 101; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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 QY 202 AACAGGTCACATCAGTCAAAATAAAATCAATTTGATTTC 243
 DB 468 AACAGGTCACATCAGTCAAAATAAAATCAATTTGATTTC 509

RESULT 10
 US-08-342-268-69
 ; Sequence 69, Application US/08342268
 ; Patent No. 5844072
 ; GENERAL INFORMATION:
 ; APPLICANT: Selsted, Michael E.
 ; APPLICANT: Ouellette, Andre J.
 ; TITLE OF INVENTION: Antibiotic Cryptdin Peptides and Methods
 ; TITLE OF INVENTION: of Their Use
 ; NUMBER OF SEQUENCES: 70
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Campbell and Flores
 ; STREET: 4370 La Jolla Village Drive, Suite 700
 ; CITY: San Diego
 ; STATE: California
 ; COUNTRY: USA
 ; ZIP: 92122
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patentin Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/342,268
 ; FILING DATE: 18-NOV-1994
 ; CLASSIFICATION: 435
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 07/930,649
 ; FILING DATE: 14-AUG-1992
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 07/889,020
 ; FILING DATE: 26-MAY-1992
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Campbell, Cathryn A.
 ; REGISTRATION NUMBER: 31,815
 ; REFERENCE/DOCKET NUMBER: P-UC 1206
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (619) 535-9001
 ; TELEFAX: (619) 535-8949
 ; INFORMATION FOR SEQ ID NO: 69:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 2408 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 US-08-342-268-69

Query Match 41.3%; Score 100.4; DB 2; Length 2408;
 Best Local Similarity 99.0%; Pred. No. 9.6e-14;
 Matches 101; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 142 CAGCTTTTATCTAAGTTGGCATTATATAAAAGCATTGCTTATCAATTTGTTGCAACG 201
 DB 408 CTGCTTTTATCTAAGTTGGCATTATATAAAAGCATTGCTTATCAATTTGTTGCAACG 467
 QY 202 AACAGGTCACATCAGTCAAAATAAAATCAATTTGATTTC 243
 DB 468 AACAGGTCACATCAGTCAAAATAAAATCAATTTGATTTC 509

RESULT 11
 US-09-015-968-69

; Sequence 69, Application US/09015968
; Patent No. 6057425
; GENERAL INFORMATION:
; APPLICANT: Selsted, Michael E.
; APPLICANT: Ouellette, Andre J.
; TITLE OF INVENTION: Antibiotic Cryptdin Peptides and Methods
; TITLE OF INVENTION: of Their Use
; NUMBER OF SEQUENCES: 70
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell and Flores
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: USA
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/015,968
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/482,279
; FILING DATE: 07-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/342,268
; FILING DATE: 18-NOV-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/930,649
; FILING DATE: 14-AUG-1992
; APPLICATION DATA:
; FILING DATE: 26-MAY-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-UC 3003
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 69:
; LENGTH: 2408 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-09-015-968-69

Query Match 41.3%; Score 100.4; DB 3; Length 2408;
Best Local Similarity 99.0%; Pred. No. 9.6e-14;
Matches 101; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 142 CAGCTTTTATCTAGTGGCATTATATAAAAGCATTGCTTATCAATTTGTTGCAAG 201
Db 408 CTGCTTTTATCTAGTGGCATTATATAAAAGCATTGCTTATCAATTTGTTGCAAG 467
QY 202 AACAGGTCACATCAGTCAAAATAAATCAATTTGTTGTTTC 243
Db 468 AACAGGTCACATCAGTCAAAATAAATCAATTTGTTGTTTC 509

RESULT 12
US-09-397-386-69
; Sequence 69, Application US/09397386
; Patent No. 6300470
; GENERAL INFORMATION:
; APPLICANT: Selsted, Michael E.
; APPLICANT: Ouellette, Andre J.
; TITLE OF INVENTION: Antibiotic Cryptdin Peptides and Methods
; TITLE OF INVENTION: of Their Use

; NUMBER OF SEQUENCES: 70
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell and Flores
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: USA
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/397,386
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/015,968
; FILING DATE:
; APPLICATION NUMBER: US 08/482,279
; FILING DATE: 07-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/342,268
; FILING DATE: 18-NOV-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/930,649
; FILING DATE: 14-AUG-1992
; APPLICATION DATA:
; FILING DATE: 26-MAY-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-UC 3003
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 69:
; LENGTH: 2408 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-09-397-386-69

Query Match 41.3%; Score 100.4; DB 4; Length 2408;
Best Local Similarity 99.0%; Pred. No. 9.6e-14;
Matches 101; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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QY 202 AACAGGTCACATCAGTCAAAATAAATCAATTTGTTGTTTC 243
Db 468 AACAGGTCACATCAGTCAAAATAAATCAATTTGTTGTTTC 509

RESULT 13
US-09-308-090-1
; Sequence 1, Application US/09308090
; Patent No. 6395963
; GENERAL INFORMATION:
; APPLICANT: Ohl, Stephan
; APPLICANT: Van Der Lee, Frederique
; APPLICANT: Goddijn, Oscar
; APPLICANT: Klap, Joke
; APPLICANT: Sijmons, Peter
; TITLE OF INVENTION: Nematode-Inducible Regulatory DNA Sequences
; FILE REFERENCE: MOG 57680
; CURRENT APPLICATION NUMBER: US/09/308,090
; CURRENT FILING DATE: 1999-05-14

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; EARLIER APPLICATION NUMBER: PCT/EP97/06472
; EARLIER FILING DATE: 1997-11-18
; EARLIER APPLICATION NUMBER: EP 96203213.2
; EARLIER FILING DATE: 1996-11-18
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 3484
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (3482)..(3484)
US-09-308-090-1

Query Match      41.3%; Score 100.4; DB 4; Length 3484;
Best Local Similarity 99.0%; Pred. No. 9.9e-14;
Matches 101; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Db 420 CTGCTTTTATCTAAGTTGGCATTATATAAAAGCATTGCTTATCAATTTGTTGCAACG 479

QY 202 AACAGGTCACATCAGTCAAAATAAAATCATTATTGATTTC 243
Db 480 AACAGGTCACATCAGTCAAAATAAAATCATTATTGATTTC 521

RESULT 14
US-09-380-090A-1
; Sequence 1, Application US/09380090A
; Patent No. 6555529
; GENERAL INFORMATION:
; APPLICANT: OHL, Stephan Andreas
; SIMONS, Peter Christiaan
; KLEIN-VAN DER LEE, Frederique
; Marianne
; GODDIJN, Oscar
; KLAIP, Joke
; TITLE OF INVENTION: NEMATODE-INDUCIBLE REGULATORY DNA
; SEQUENCES
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hale and Dorr LLP
; STREET: 60 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: United States
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/380,090A
; FILING DATE: 17-May-1999
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/EP97/06472
; FILING DATE: 18-NOV-1997
; APPLICATION NUMBER: EP 96203213.2
; FILING DATE: 18-NOV-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Superko, Colleen
; REGISTRATION NUMBER: 39,850
; REFERENCE/DOCKET NUMBER: SYN-010
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 526-6000
; TELEFAX: (617) 526-5000
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3484 base pairs
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; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Arabidopsis thaliana
; STRAIN: C24
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 3481..3484
; OTHER INFORMATION: /codon_start= 3482
; SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-380-090A-1

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Best Local Similarity 99.0%; Pred. No. 9.9e-14;
Matches 101; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 142 CAGCTTTTATCTAAGTTGGCATTATATAAAAGCATTGCTTATCAATTTGTTGCAACG 201
Db 420 CTGCTTTTATCTAAGTTGGCATTATATAAAAGCATTGCTTATCAATTTGTTGCAACG 479

QY 202 AACAGGTCACATCAGTCAAAATAAAATCATTATTGATTTC 243
Db 480 AACAGGTCACATCAGTCAAAATAAAATCATTATTGATTTC 521

RESULT 15
US-09-016-366A-13
; Sequence 13, Application US/09016366A
; Patent No. 5953431
; GENERAL INFORMATION:
; APPLICANT: Stevens, Richard L.
; APPLICANT: Huang, Chifu
; TITLE OF INVENTION: MAST CELL PROTEASE PEPTIDE
; TITLE OF INVENTION: INHIBITORS
; NUMBER OF SEQUENCES: 65
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Wolf, Greenfield & Sacks, P.C.
; STREET: 600 Atlantic Avenue
; CITY: Boston
; STATE: MA
; COUNTRY: U.S.A.
; ZIP: 02210-2211
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/016,366A
; FILING DATE: January 30, 1998
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/037,090
; FILING DATE: 05-FEB-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Plumer, Elizabeth R.
; REGISTRATION NUMBER: 36,637
; REFERENCE/DOCKET NUMBER: B0801/7093
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-720-3500
; TELEFAX: 617-720-2441
; TELEX:
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3757 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

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(without alignments)
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Title: US-10-082-772B-2

Perfect score: 243

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Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0

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Post-processing: Minimum Match 0%

Maximum Match 100%

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14: gb.vi.*

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19: em.mu.*

20: em.cm.*

21: em.or.*

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33: em.htg_mus.*

34: em.htg_pln.*

35: em.htg_rod.*

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37: em.htg_vrt.*

38: em_sy.*

39: em_htgo_hum.*

40: em_htgo_mus.*

41: em_htgo_other.*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
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5	243	100.0	1763	6	BD225932	Immediate
6	243	100.0	2758	3	PEAHRPC	M17028 P.falciparu
7	243	100.0	3485	12	AF178449	AF178449 Integrati
8	243	100.0	3485	12	AF178450	Integrati
9	243	100.0	4105	12	AF271663	AF271663 Cloning v
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13	243	100.0	5641	6	AX113748	AX113748 Sequence
14	243	100.0	5670	6	AX113749	AX113749 Sequence
15	243	100.0	5826	6	AX113746	AX113746 Sequence
16	243	100.0	6000	12	U66308	U66308 Expression
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19	243	100.0	6071	6	AX113747	AX113747 Sequence
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22	243	100.0	42530	12	CVU39285	U39285 Cloning vec
23	243	100.0	42531	12	CVU39286	U39286 Cloning vec
24	243	100.0	42704	12	CVU37692	U37692 Cloning vec
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26	241.4	99.3	243	6	AX092116	AX092116 Sequence
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30	231	95.1	4782	12	AY048740	AY048740 CRIM plas
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34	231	95.1	5771	12	AY150262	AY150262 CRIM plas
35	231	95.1	5814	12	AY150265	AY150265 CRIM plas
36	231	95.1	5911	12	AY150268	AY150268 CRIM plas
37	231	95.1	5948	12	AY054373	AY054373 CRIM plas
38	231	95.1	5986	12	AY150264	AY150264 CRIM plas
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45	226.8	93.3	4208	6	BD263379	BD263379 Compositi

ALIGNMENTS

RESULT 1	AX092113	AX092113	243 bp	DNA	linear	PAT 21-MAR-2001
LOCUS	Sequence 2 from Patent WO0116345.					
DEFINITION	AX092113					
ACCESSION	AX092113					
VERSION	AX092113.1	GI:13444356				
KEYWORDS						
SOURCE	Bacteriophage lambda					
ORGANISM	Bacteriophage lambda					
REFERENCE	Viruses; dsDNA viruses, no RNA stage; Caudovirales; Siphoviridae;					
AUTHORS	Lambda-like viruses.					
TITLE	1					
JOURNAL	Drooge, P.					
	Sequence-specific dna recombination in eukaryotic cells					
	Patent: WO 0116345-A 2 08-MAR-2001;					

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Best Local Similarity 100.0%; Pred. No. 8.9e-34;
Matches 243; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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DB 1 TCTGTTACAGGTCACCTAATACCATCTAAAGTAGTGTGATTCATAGTGCATGCTCATCTGTG 60
QY 61 TTTTACAGTATTATGATGCTCTGTTTTTATGCAAAATCTAAATTTAATATATTGATATTTA 120
DB 61 TTTTACAGTATTATGATGCTCTGTTTTTATGCAAAATCTAAATTTAATATATTGATATTTA 120
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QY 181 GCTTATCAATTTGTTGCAACGACAGGTCACCTATCAGTCAAAATATAAATCATTATTGAT 240
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QY 241 TTC 243
DB 241 TTC 243

RESULT 2
LOCUS      LAMINTATT      361 bp      DNA      linear      PHG 28-APR-1993
DEFINITION      Bacteriophage lambda int gene region.
ACCESSION      M23841
VERSION      M23841.1 GI:215177
KEYWORDS      site-specific recombination.
SOURCE      Bacteriophage lambda
ORGANISM      Bacteriophage lambda
               Viruses; dsDNA viruses, no RNA stage; Caudovirales; Siphoviridae;
               Lambda-like viruses.
REFERENCE      1 (bases 1 to 361).
AUTHORS      Schmeissner, U., McKenney, K., Rosenberg, M. and Court, D.
TITLE      Removal of a terminator structure by RNA processing regulates int
               gene expression
JOURNAL      J. Mol. Biol. 176 (1), 39-53 (1984)
MEDLINE      84242838
PUBMED      6234400
COMMENT      Original source text: Bacteriophage lambda DNA.
FEATURES      Location/Qualifiers
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               /organism="Bacteriophage lambda"
               /mol_type="genomic DNA"
               /db_xref="taxon:10710"
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Query Match      100.0%; Score 243; DB 7; Length 361;
Best Local Similarity 100.0%; Pred. No. 8.2e-34;
Matches 243; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TCTGTTACAGTCACTAATACCATCTAAAGTAGTGTGATTCATAGTGCATGCTCATCTGTG 60
DB 259 TCTGTTACAGTCACTAATACCATCTAAAGTAGTGTGATTCATAGTGCATGCTCATCTGTG 200
QY 61 TTTTACAGTATTATGATGCTCTGTTTTTATGCAAAATCTAAATTTAATATATTGATATTTA 120
DB 199 TTTTACAGTATTATGATGCTCTGTTTTTATGCAAAATCTAAATTTAATATATTGATATTTA 140
QY 121 TATCATTTTACGTTTCTGCTGCTGCTTTTATCTACTAGTGGCATTTAAAAAGCATT 180
DB 121 TATCATTTTACGTTTCTGCTGCTGCTTTTATCTACTAGTGGCATTTAAAAAGCATT 180

FEATURES
  source      Droege, Peter (DE)
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               1..243
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Query Match      100.0%; Score 243; DB 6; Length 243;
Best Local Similarity 100.0%; Pred. No. 7.3e-34;
Matches 243; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TCTGTTACAGGTCACCTAATACCATCTAAAGTAGTGTGATTCATAGTGCATGCTCATCTGTG 60
DB 139 TCTGTTACAGGTCACCTAATACCATCTAAAGTAGTGTGATTCATAGTGCATGCTCATCTGTG 198
QY 61 TTTTACAGTATTATGATGCTCTGTTTTTATGCAAAATCTAAATTTAATATATTGATATTTA 120
DB 199 TTTTACAGTATTATGATGCTCTGTTTTTATGCAAAATCTAAATTTAATATATTGATATTTA 258
QY 121 TATCATTTTACGTTTCTGCTGCTGCTTTTATCTACTAGTGGCATTTAAAAAGCATT 180
DB 259 TATCATTTTACGTTTCTGCTGCTGCTTTTATCTACTAGTGGCATTTAAAAAGCATT 318
QY 181 GCTTATCAATTTGTTGCAACGACAGGTCACCTATCAGTCAAAATATAAATCATTATTGAT 240
DB 319 GCTTATCAATTTGTTGCAACGACAGGTCACCTATCAGTCAAAATATAAATCATTATTGAT 378
QY 241 TTC 243
DB 379 TTC 381

RESULT 3
LOCUS      AX101000      610 bp      DNA      linear      PAT 10-APR-2001
DEFINITION      Sequence 1 from Patent WO0121780.
ACCESSION      AX101000
VERSION      AX101000.1 GI:13619857
KEYWORDS      Nicotiana tabacum (common tobacco)
SOURCE      Nicotiana tabacum
ORGANISM      Nicotiana tabacum
               Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
               Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
               asterids; lamiids; Solanales; Solanaceae; Nicotiana.
REFERENCE      1
AUTHORS      Meyer, P.L. and Zubko, E.L.
TITLE      Targeted gene removal
JOURNAL      Patent: WO 0121780-A 1 29-MAR-2001;
               THE UNIVERSITY OF LEEDS (GB)
FEATURES      Location/Qualifiers
               1..610
               /organism="Nicotiana tabacum"
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               /db_xref="taxon:4097"
ORIGIN
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Best Local Similarity 100.0%; Pred. No. 7.3e-34;
Matches 243; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TCTGTTACAGGTCACCTAATACCATCTAAAGTAGTGTGATTCATAGTGCATGCTCATCTGTG 60
DB 139 TCTGTTACAGGTCACCTAATACCATCTAAAGTAGTGTGATTCATAGTGCATGCTCATCTGTG 198
QY 61 TTTTACAGTATTATGATGCTCTGTTTTTATGCAAAATCTAAATTTAATATATTGATATTTA 120
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DB 259 TATCATTTTACGTTTCTGCTGCTGCTTTTATCTACTAGTGGCATTTAAAAAGCATT 318
QY 181 GCTTATCAATTTGTTGCAACGACAGGTCACCTATCAGTCAAAATATAAATCATTATTGAT 240
DB 319 GCTTATCAATTTGTTGCAACGACAGGTCACCTATCAGTCAAAATATAAATCATTATTGAT 378
QY 241 TTC 243
DB 379 TTC 381

RESULT 4
LOCUS      MACHSS/c      1668 bp      mRNA      linear      PRI 06-FEB-1999
DEFINITION      Macaca fascicularis mRNA for hydroxysteroid sulfotransferase
               subunit, complete cds.
ACCESSION      D85521
VERSION      D85521.1 GI:1345405
KEYWORDS      hydroxysteroid sulfotransferase subunit.
SOURCE      Macaca fascicularis (crab-eating macaque)
ORGANISM      Macaca fascicularis
               Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
               Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
               Cercopithecinae; Macaca.

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REFERENCE 1 (bases 1 to 1668)
AUTHORS Ogura,K., Satsukawa,M., Kato,K., Okuda,H. and Watabe,T.
TITLE Molecular cloning of monkey liver hydroxysteroid sulfotransferase
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 1668)
AUTHORS Ogura,K.
TITLE Direct Submission
JOURNAL Submitted (23-MAY-1996) Kenichiro Ogura, Tokyo University of
Pharmacy and Life Science, Department of Drug Metabolism and
Molecular Toxicology; 1432-1 Horinouchi, Hachioji, Tokyo 192-0392,
Japan (E-mail:ogurak@ps.toyaku.ac.jp, Tel:+81-426-76-4518,
Fax:+81-426-76-4517)
FEATURES
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    1..1668
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        611..1468
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            GSWFDIHGMMPREKNFLLSYELKQDTRTVEKICQFLGKLEPELNLILKNS
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        QY 61 TTTTACAGTATTATGAGTCTGTTTTTATGCAAAATCTAATTAATATATGATATTTA 120
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        Db 331 TTTTACAGTATTATGAGTCTGTTTTTATGCAAAATCTAATTAATATATGATATTTA 272

        QY 121 TATCATTTTACGTTCTCGTTCAGCTTTTATATCTAAGTTGGCATTATATAAAAGCATT 180
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        Db 271 TATCATTTTACGTTCTCGTTCAGCTTTTATATCTAAGTTGGCATTATATAAAAGCATT 212

        QY 181 GCTTATCAATTTGTTGCAACGACGTCATCTATCAGTCAAAATATAATCATTTTGTAT 240
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        Db 211 GCTTATCAATTTGTTGCAACGACGTCATCTATCAGTCAAAATATAATCATTTTGTAT 252

        QY 241 TTC 243
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        Db 151 TTC 149

    RESULT 5
    BD225932/c
    LOCUS BD225932 1763 bp DNA linear PAT 17-JUL-2003
    DEFINITION Immediate early gene and method for using the same.
    ACCESSION BD225932
    VERSION BD225932.1 GI:33035702
    KEYWORDS JP 2002512772-A/49.
    SOURCE Rattus norvegicus (Norway rat)
    ORGANISM Rattus norvegicus
        Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
        Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
        Rattus.
    REFERENCE 1 (bases 1 to 1763)
    AUTHORS Worley,P.F., Lanahan,A., Goetz,B., Hiemisch,H., Kuner,R.,

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Scheek,S., Nikolich,K. and Zhukovski,E.
Immediate early gene and method for using the same
Patent: JP 2002512772-A 49 08-MAY-2002;
THE JOHNS HOPKINS UNIVERSITY SCHOOL OF MEDICINE, BASF LYNX
BIOSCIENCE AG
OS Rattus norvegicus (rat)
PN JP 2002512772-A/49
PD 08-MAY-2002
PF 05-FEB-1999 JP 2000530634
PR 09-FEB-1998 US 60/074135,12-FEB-1998 US 60/074518 PI
PAUL F WORLEY, ANTHONY LANAHAN, BERNARD GOETZ, HOLGER HIEMISCH, PI
ROHINI KUNER.
PI SIGRID SCHEEK, KAROLY NIKOLICH, EUGENE ZHUKOVSKI PC
C12N15/09, A61K31/711, A61K48/00, A61P25/00, A61P25/28, C07H21/04, PC
C07K14/47,
PC C07K16/18, C12N1/15, C12N1/19, C12N1/21, C12N5/10, C12P21/08 PC
C12Q1/68, G01N33/53,
PC C12N15/00, C12N5/00
CC n is either a, t, g, or c
FH Key Location/Qualifiers
FT misc feature (1)..(1763).
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        Query Match          100.0%; Score 243; DB 6; Length 1763;
        Best Local Similarity 100.0%; Pred. No. 5.9e-34;
        Matches 243; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

        QY 1 TCTGTTACAGGTCACCTAATACCTAAGTAGTGTGATTCATAGTGCATATGTTGTG 60
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        Db 431 TCTGTTACAGGTCACCTAATACCTAAGTAGTGTGATTCATAGTGCATATGTTGTG 372

        QY 61 TTTTACAGTATTATGAGTCTGTTTTTATGCAAAATCTAATTAATATATGATATTTA 120
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        Db 371 TTTTACAGTATTATGAGTCTGTTTTTATGCAAAATCTAATTAATATATGATATTTA 312

        QY 121 TATCATTTTACGTTCTCGTTCAGCTTTTATATCTAAGTTGGCATTATATAAAAGCATT 180
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        Db 311 TATCATTTTACGTTCTCGTTCAGCTTTTATATCTAAGTTGGCATTATATAAAAGCATT 252

        QY 181 GCTTATCAATTTGTTGCAACGACGTCATCTATCAGTCAAAATATAATCATTTTGTAT 240
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        Db 251 GCTTATCAATTTGTTGCAACGACGTCATCTATCAGTCAAAATATAATCATTTTGTAT 292

        QY 241 TTC 243
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        Db 191 TTC 189

    RESULT 6
    PFAHRPC/c
    LOCUS PFAHRPC 2758 bp DNA linear INV 26-APR-1993
    DEFINITION P.falciiparum histidine-rich protein genes.
    ACCESSION M17028
    VERSION M17028.1 GI:160339
    KEYWORDS histidine-rich protein,
    SOURCE Plasmodium falciparum (malaria parasite P. falciparum)
    ORGANISM Plasmodium falciparum
        Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
    REFERENCE 1 (bases 1 to 2758)
    AUTHORS Lenstra,R., d'Auric,I., Andrieu,B., Le Bras,J. and Galibert,F.
    TITLE Cloning and sequencing of Plasmodium falciparum DNA fragments
    containing repetitive regions potentially coding for histidine-rich
    proteins: identification of two overlapping reading frames
    JOURNAL Biochem. Biophys. Res. Commun. 146 (1), 368-377 (1987)
    MEDLINE 8720765
    PUBMED 3038111
    COMMENT Original source text: P.falciiparum, cDNA to mRNA, clone M4.
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        Location/Qualifiers

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Matches 243; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCTGTTACAGGTCACTAATACCATCTAAGTAGTTCATGATTCAGTCGATATGTTGTG 60
DB 2548 TCTGTTACAGGTCACTAATACCATCTAAGTAGTTCATGATTCAGTCGATATGTTGTG 2489

QY 61 TTTTACAGTATATAGTCTGTTTATGCAAAATCTAATTAATATATGATATTA 120
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QY 121 TATCATTTTACGTTTCTCGTTTCAGCTTTTATATACTAAGTTGGCATTATAAAAAGCATT 180
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QY 181 GCTTATCAATTTGTTGCAACGAACAGGTCACCTATCAGTCACAAATAAAATCATTATTGAT 240
DB 2368 GCTTATCAATTTGTTGCAACGAACAGGTCACCTATCAGTCACAAATAAAATCATTATTGAT 2309

QY 241 TTC 243
DB 2308 TTC 2306

RESULT 7
AF178449
LOCUS
DEFINITION
AF178449 3485 bp DNA linear SYN 20-JUL-2000
and beta-galactosidase alpha peptide (lacZa) genes, complete cds.
ACCESSION
AF178449
VERSION
AF178449.1 GI:9294785
KEYWORDS
Integration vector pCDilPKS
Integration vector pCDilPKS
artificial sequences: vectors.
REFERENCE
1 (bases 1 to 3485)
Platt,R., Drescher,C., Park,S.K. and Phillips,G.J.
AUTHORS
Genetic system for reversible integration of DNA constructs and
TITLE
lacZ gene fusions into the Escherichia coli chromosome
JOURNAL
Plasmid 43 (1), 12-23 (2000)
MEDLINE
20079288
PUBMED
10610816
REFERENCE
2 (bases 1 to 3485)
Platt,R., Drescher,C., Park,S.K. and Phillips,G.J.
AUTHORS
Direct Submision
TITLE
Submitted (18-AUG-1999) Microbiology, Iowa State University, 207
JOURNAL
Science I Building, Ames, IA 50011, USA
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668..915
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Matches 243; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCTGTTACAGTCACTAATACCATCTAAGTAGTGAATTCATAGTGAATGATATGTTGTG 60
Db 673 TCTGTTACAGTCACTAATACCATCTAAGTAGTGAATTCATAGTGAATGATATGTTGTG 732

Qy 61 TTTTACAGTATTATGAGTCTGTTTTTATGCAAAATCTAATTTAATATATGATATTTA 120
Db 733 TTTTACAGTATTATGAGTCTGTTTTTATGCAAAATCTAATTTAATATATGATATTTA 792

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Db 793 TATCATTTTACGTTTCGTTTCAGTTTCTTTTATCTAAGTTGGCATTTAAAAAGCATT 852

Qy 181 GCTTATCAATTTGTTGCAACGACAGTCACTATCAGTCAAAATCAATTTAATATGATATTTA 240
Db 853 GCTTATCAATTTGTTGCAACGACAGTCACTATCAGTCAAAATCAATTTAATATGATATTTA 912

Qy 241 TTC 243
Db 913 TTC 915

RESULT 8
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LOCUS
DEFINITION
Integration vector pCD11PSK chloramphenicol transacetylase (cat)
and beta-galactosidase alpha peptide (lacZa) genes, complete cds.
ACCESSION
AF178450
VERSION
AF178450.1 GI:9294788
KEYWORDS
Integration vector pCD11PSK
SOURCE
Integration vector pCD11PSK
ORGANISM
artificial sequences; vectors.
REFERENCE
1 (bases 1 to 3485)
Platt,R., Drescher,C., Park,S.K. and Phillips,G.J.
Genetic system for reversible integration of DNA constructs and
lacZ gene fusions into the Escherichia coli chromosome
JOURNAL
Plasmid 43 (1), 12-23 (2000)
MEDLINE
20079288
PUBMED
10610816
REFERENCE
2 (bases 1 to 3485)
Platt,R., Drescher,C., Park,S.K. and Phillips,G.J.
Direct Submission
TITLE
Submitted (18-AUG-1999) Microbiology, Iowa State University, 207
Science I Building, Ames, IA 50011, USA
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ORIGIN
Query Match      100.0%; Score 243; DB 12; Length 3485;
Best Local Similarity 100.0%; Pred. No. 5.2e-34;
Matches 243; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCTGTTACAGTCACTAATACCATCTAAGTAGTGAATTCATAGTGAATGATATGTTGTG 60
Db 673 TCTGTTACAGTCACTAATACCATCTAAGTAGTGAATTCATAGTGAATGATATGTTGTG 732

Qy 61 TTTTACAGTATTATGAGTCTGTTTTTATGCAAAATCTAATTTAATATATGATATTTA 120
Db 733 TTTTACAGTATTATGAGTCTGTTTTTATGCAAAATCTAATTTAATATATGATATTTA 792

Qy 121 TATCATTTTACGTTTCGTTTCAGTTTCTTTTATCTAAGTTGGCATTTAAAAAGCATT 180
Db 793 TATCATTTTACGTTTCGTTTCAGTTTCTTTTATCTAAGTTGGCATTTAAAAAGCATT 852

Qy 181 GCTTATCAATTTGTTGCAACGACAGTCACTATCAGTCAAAATCAATTTAATATGATATTTA 240
Db 853 GCTTATCAATTTGTTGCAACGACAGTCACTATCAGTCAAAATCAATTTAATATGATATTTA 912

Qy 241 TTC 243
Db 913 TTC 915

RESULT 9
AF271663      4105 bp DNA circular SYN 11-JUL-2000
LOCUS
DEFINITION
Cloning vector pLDR9, complete sequence.
ACCESSION
AF271663
VERSION
AF271663.1 GI:9022390
KEYWORDS
Cloning vector pLDR9
SOURCE
Cloning vector pLDR9
ORGANISM
artificial sequences; vectors.
REFERENCE
1 (bases 1 to 4105)
Wiencis,A.M., Keagle,P., Andersen,J., Wotanis,J., Newcombe,R. and
August,P.R.
Direct Submission
TITLE
Submitted (24-MAY-2000) Molecular Genomics, Aventis
Pharmaceuticals, 26 Landsdowne Street, Cambridge, MA 02139, USA
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Location/Qualifiers
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CDS

CDS

misc_feature

ORIGIN

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 Best Local Similarity 100.0%; Pred. No. 5e-34; 0; Indels 0; Gaps 0;
 Matches 243; Conservative 0; Mismatches 0;

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 Db 2617 TCTGTTACAGGTCACATAACCATCTAAGTAGTTGATTCATAGTGAATGATGTTGG 2676
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 Db 2677 TTTTACAGTATTATGATGATCTCTTTTATGCAAAATCTAATTTAATATATGATTTA 2736
 QY 121 TATCATTTTACGTTCTGCTTCAGCTTTTATCTAAGTTCGCTATATAAAAAGCATT 180
 Db 2737 TATCATTTTACGTTCTGCTTCAGCTTTTATCTAAGTTCGCTATATAAAAAGCATT 2796
 QY 181 GCTTATCAATTTGTTGCAACGAGGTCATCATCAGTCAAAATATAAATCATTTTGGAT 240
 Db 2797 GCTTATCAATTTGTTGCAACGAGGTCATCATCAGTCAAAATATAAATCATTTTGGAT 2856
 QY 241 TTC 243
 Db 2857 TTC 2859

RESULT 10
 XXU13848/C
 LOCUS XXU13848 4190 bp DNA circular SYN 13-DEC-1994
 DEFINITION pEXcell cloning vector, complete sequence.
 ACCESSION U13848
 VERSION U13848.1 GI:595702
 KEYWORDS T7 promoter; SP6 promoter; beta-lactamase, lacZ alpha peptide, attP.
 SOURCE unidentified cloning vector
 ORGANISM artificial sequences; vectors.
 REFERENCE 1 (bases 1 to 4190)
 AUTHORS Malone, J.A.
 TITLE pEXCell: A multifunctional cloning vector that is released from
 lambda ExCell by in vivo excision
 JOURNAL Unpublished (1994)
 REFERENCE 2 (bases 1 to 4190)

AUTHORS Malone, J.A.
 TITLE Direct Submission
 JOURNAL Submitted (19-AUG-1994) James A. Malone, International Technical
 Services, Molecular Biology Reagents Division, Pharmacia Biotech
 Inc., 2202 N. Bartlett Ave., Milwaukee, WI 53202-1009, USA

FEATURES

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 2013. .2033
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 2073. .2089
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 2097. .2154
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 the first base of the newly synthesized single strand"
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CDS

rep_origin

gene

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CDS

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misc_feature

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promoter

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ORIGIN

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Best Local Similarity 100.0%; Pred. No. 5e-34;
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Db 4029 TTTTACAGTATTATGTAAGTCTGTTTTTATGCAAAATCTAATTAATATATGATATTTA 3970

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Db 3969 TATCATTTTACGTTCTCGTTACGTTTATATACCTAGTTGGCATATATAAAGCAATT 3910

QY 181 GCATTATCAATTTGTTGCAAGCAAGTCACATCATCAGTCACAAATATAAATCATTTTGCAT 240
Db 3909 GCATTATCAATTTGTTGCAAGCAAGTCACATCATCAGTCACAAATATAAATCATTTTGCAT 3850

QY 241 TTC 243
Db 3849 TTC 3847

RESULT 11
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LOCUS      4549 bp      DNA      linear      SYN 20-JUL-2000
DEFINITION Integration vector pCD13PKS aminoglycoside adenylyltransferase (aadA)
            and beta-galactosidase alpha peptide (lacZa) genes, complete cds.
ACCESSION AF178452
VERSION    AF178452.1 GI:9294794
KEYWORDS   Integration vector pCD13PKS
SOURCE     Integration vector pCD13PKS
ORGANISM   Integration vector pCD13PKS
REFERENCE  1 (bases 1 to 4549)
AUTHORS    Platt,R., Drescher,C., Park,S.K. and Phillips,G.J.
TITLE      Genetic system for reversible integration of DNA constructs and
            lacZ gene fusions into the Escherichia coli chromosome
JOURNAL    Plasmid 43 (1), 12-23 (2000)
MEDLINE    20079288
PUBMED     10610816
REFERENCE  2 (bases 1 to 4549)
AUTHORS    Platt,R., Drescher,C., Park,S.K. and Phillips,G.J.
TITLE      Direct Submission
JOURNAL    Submitted (18-AUG-1999) Microbiology, Iowa State University, 207
            Science I Building, Ames, IA 50011, USA
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CDS         complement(1798..2652)
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Best Local Similarity 100.0%; Pred. No. 4.9e-34;
Matches 243; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCTGTTACAGGTCACCTAATACCATCTAAGTAGTGTGATTCATAGTACGCTGCATATGTTGTG 60
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Db 733 TTTTACAGTATTATGTAAGTCTGTTTTTATGCAAAATCTAATTAATATATGATATTTA 792

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QY 181 GCATTATCAATTTGTTGCAAGCAAGTCACATCATCAGTCACAAATATAAATCATTTTGCAT 240
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QY 241 TTC 243
Db 913 TTC 915

RESULT 12
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LOCUS      4549 bp      DNA      linear      SYN 20-JUL-2000
DEFINITION Integration vector pCD13PKS aminoglycoside adenylyltransferase (aadA)
            and beta-galactosidase alpha peptide (lacZa) genes, complete cds.
ACCESSION AF178453
VERSION    AF178453.1 GI:9294797
KEYWORDS   Integration vector pCD13PKS
SOURCE     Integration vector pCD13PKS
ORGANISM   Integration vector pCD13PKS
REFERENCE  1 (bases 1 to 4549)
AUTHORS    Platt,R., Drescher,C., Park,S.K. and Phillips,G.J.
TITLE      Genetic system for reversible integration of DNA constructs and
            lacZ gene fusions into the Escherichia coli chromosome
JOURNAL    Plasmid 43 (1), 12-23 (2000)
MEDLINE    20079288
PUBMED     10610816
REFERENCE  2 (bases 1 to 4549)
AUTHORS    Platt,R., Drescher,C., Park,S.K. and Phillips,G.J.
TITLE      Direct Submission
JOURNAL    Submitted (18-AUG-1999) Microbiology, Iowa State University, 207
            Science I Building, Ames, IA 50011, USA
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 QY 61 TTTTACAGTATATAGTCTGCTTTTATGCAAAATCTAATTAATATATGATTTA 120
 Db 733 TTTTACAGTATATAGTCTGCTTTTATGCAAAATCTAATTAATATATGATTTA 792
 QY 121 TATCATTTTACGTTCTCGTTCAGCTTTTATATCTAAGTTGGCATTATAAAAAGCATT 180
 Db 793 TATCATTTTACGTTCTCGTTCAGCTTTTATATCTAAGTTGGCATTATAAAAAGCATT 852
 QY 181 GCTTATCAATTTGTTGCAACGACAGGTCACCTATCAGTCAAAATATAAATCATTATTGAT 240
 Db 853 GCTTATCAATTTGTTGCAACGACAGGTCACCTATCAGTCAAAATATAAATCATTATTGAT 912
 QY 241 TTC 243
 Db 913 TTC 915

RESULT 13
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 DEFINITION Sequence 13 from Patent WO0127322.
 ACCESSION AX113748
 VERSION AX113748.1 GI:13939915
 KEYWORDS
 SOURCE synthetic construct
 ORGANISM synthetic construct
 artificial sequences.
 REFERENCE 1
 AUTHORS Zyskind, J.
 TITLE Chitobiose as a reporter enzyme
 JOURNAL Patent: WO 0127322-A 13 19-APR-2001;
 Elitra Pharmaceuticals, Inc. (US)
 FEATURES Location/Qualifiers

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 QY 1 TCTGTTACAGGTCACCTAATACCATCTAAGTAGTTGATTCATAGTCGACATGTCATATGTTG 60
 Db 4703 TCTGTTACAGGTCACCTAATACCATCTAAGTAGTTGATTCATAGTCGACATGTCATATGTTG 4762
 QY 61 TTTTACAGTATATAGTCTGCTTTTATGCAAAATCTAATTAATATATGATTTA 120
 Db 4763 TTTTACAGTATATAGTCTGCTTTTATGCAAAATCTAATTAATATATGATTTA 4822
 QY 121 TATCATTTTACGTTCTCGTTCAGCTTTTATATCTAAGTTGGCATTATAAAAAGCATT 180
 Db 4823 TATCATTTTACGTTCTCGTTCAGCTTTTATATCTAAGTTGGCATTATAAAAAGCATT 4882
 QY 181 GCTTATCAATTTGTTGCAACGACAGGTCACCTATCAGTCAAAATATAAATCATTATTGAT 240
 Db 4883 GCTTATCAATTTGTTGCAACGACAGGTCACCTATCAGTCAAAATATAAATCATTATTGAT 4942
 QY 241 TTC 243
 Db 4943 TTC 4945

RESULT 14
 LOCUS AX113749/c 5670 bp DNA linear PAT 01-MAY-2001
 DEFINITION Sequence 14 from Patent WO0127322.
 ACCESSION AX113749
 VERSION AX113749.1 GI:13939916
 KEYWORDS
 SOURCE synthetic construct
 ORGANISM synthetic construct
 artificial sequences.
 REFERENCE 1
 AUTHORS Zyskind, J.
 TITLE Chitobiose as a reporter enzyme
 JOURNAL Patent: WO 0127322-A 14 19-APR-2001;
 Elitra Pharmaceuticals, Inc. (US)
 FEATURES Location/Qualifiers
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 Best Local Similarity 100.0%; Pred. No. 4.7e-34;
 Matches 243; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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 Db 4981 TTTTACAGTATATAGTCTGCTTTTATGCAAAATCTAATTAATATATGATTTA 4922
 QY 121 TATCATTTTACGTTCTCGTTCAGCTTTTATATCTAAGTTGGCATTATAAAAAGCATT 180
 Db 4921 TATCATTTTACGTTCTCGTTCAGCTTTTATATCTAAGTTGGCATTATAAAAAGCATT 4862
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Db 4861 GCTTATCAATTTCTGCAACGACAGTGCTATCATCAGTCAAAATAAAATCATTATTGAT 4802
 QY 241 TTC 243
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 Db 4801 TTC 4799

RESULT 15
 AX113746
 LOCUS AX113746 5826 bp DNA linear PAT 01-MAY-2001
 DEFINITION Sequence 11 from Patent WO0127322.
 ACCESSION AX113746
 VERSION AX113746.1 GI:13939913
 KEYWORDS
 SOURCE synthetic construct
 ORGANISM synthetic construct
 artificial sequences.
 REFERENCE 1
 AUTHORS Zyskind, J.
 TITLE Chitinase as a reporter enzyme
 JOURNAL Patent: WO 0127322-A 11 19-APR-2001;
 Elitra Pharmaceuticals, Inc. (US)
 FEATURES
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 /mol_type="unassigned DNA"
 /db_xref="taxon:32630"
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ORIGIN

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 QY 61 TTTTACAGTATTATGATGCTGTTTTTTATGCAAAATCTAATTTAATATATATGATATTTA 120
 Db 4948 TTTTACAGTATTATGATGCTGTTTTTTATGCAAAATCTAATTTAATATATATGATATTTA 5007
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 QY 241 TTC 243
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 Db 5128 TTC 5130

Search completed: September 9, 2004, 19:34:29
 Job time : 1679.36 secs

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OM nucleic - nucleic search, using sw model

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Title: US-10-082-772B-2

Perfect score: 243

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Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 3373863 seqs, 2124099041 residues

Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

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- 6: Geneseqn2002s:*
- 7: Geneseqn2003as:*
- 8: Geneseqn2003bs:*
- 9: Geneseqn2003cs:*
- 10: Geneseqn2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	243	100.0	248	8 ACC85316	Acc85316 Recombina
3	243	100.0	282	7 ACC44676	Acc44676 Murine rD
4	243	100.0	282	7 ABT16636	Abt16636 Artificia
5	243	100.0	610	5 AAF79770	Aaf79770 Bacteriop
6	243	100.0	1469	7 ABQ80306	Abq80306 Lambda fr
7	243	100.0	1469	7 ACC83020	Acc83020 Bacteriop
8	243	100.0	1763	2 AAZ30709	Aaz30709 Rat neuro
9	243	100.0	4346	7 ACC44716	Acc44716 Plasmid p
10	243	100.0	4346	7 ABT16615	Abt16615 Artificia
11	243	100.0	4909	2 AAT18924	Aat18924 Plasmid p
12	243	100.0	5641	4 AAF30800	Aaf30800 Vector pl
13	243	100.0	5670	4 AAF30801	Aaf30801 Vector pl
14	243	100.0	5826	4 AAF30798	Aaf30798 Vector pl
15	243	100.0	6071	4 AAF30799	Aaf30799 Vector pl
16	243	100.0	7652	2 AAQ45682	Aaq45682 Sequencin
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18	226.8	93.3	4165	3 AAC55524	Aac55524 Donor pla
19	226.8	93.3	4204	3 AAC55522	Aac55522 Donor pla
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21	226.8	93.3	4470	3 AAC55521	Aac55521 Donor pla
22	226.8	93.3	4470	7 ABZ58767	Abz58767 Destinati
23	226.8	93.3	4892	8 ADA50329	Ada50329 Plasmid v

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	25	226.8	93.3	5156	3 AAC55526	Aac55526 Donor pla
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	36	225.4	92.8	4470	3 AAC55521	Aac55521 Donor pla
	37	225.4	92.8	4470	7 ABZ58767	Abz58767 Destinati
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	39	225.4	92.8	4892	8 ADA50329	Ada50329 Plasmid v
	40	225.4	92.8	4939	3 AAC55525	Aac55525 Donor pla
c	41	225.4	92.8	5584	3 AAC55632	Aac55632 Donor pla
	42	225.4	92.8	5584	7 ABZ58766	Abz58766 Donor pla
c	43	225.2	92.7	4165	3 AAC55524	Aac55524 Donor pla
c	44	225.2	92.7	5156	3 AAC55526	Aac55526 Donor pla
c	45	225	92.6	233	3 AAC55383	Aac55383 Recombina

ALIGNMENTS

RESULT 1
AAF61418
ID AAF61418 standard; DNA; 243 BP.
XX
AC AAF61418;
XX
DT 05-JUN-2001 (first entry)
XX
DE Bacteriophage lambda attP DNA fragment.
XX
KW Sequence-specific recombination; SSR; integrase; gene therapy; somatic;
KW targeted integration; attP; ds.
XX
OS Bacteriophage lambda.
XX
BN DE19941186-Al.
XX
PD 01-MAR-2001.
XX
PF 30-AUG-1999; 99DE-01041186.
XX
PR 30-AUG-1999; 99DE-01041186.
XX
PA (DROE/) DROEGE P.
XX
PI Droege P;
XX
DR WPI; 2001-246016/26.
XX
FT Sequence-specific recombination of DNA in eukaryotes, useful particularly
FT for somatic cell gene therapy, uses an integrase to effect recombination
FT between att sites.
XX
PS Claim 2; Page 13; 24pp; German.
XX
CC This invention describes a novel sequence-specific recombination (SSR) of
CC DNA in a eukaryotic cell, comprising introducing two DNA sequences (I,
CC II) into a cell, using an integrase (Int) to effect SSR. The invention
CC also describes (1) a nucleic acid comprising a 243 base pair sequence
CC (III), fully defined in the specification, or its derivatives; and (2)
CC vector containing (III), or its derivatives, plus a therapeutic gene, or
CC its derivatives. The method is particularly used in somatic gene therapy
CC in humans and animals, but can be applied more generally for gene
CC transfer to animal or plant cells. The method is simple and controllable,
CC and provides stable and targeted integration of selected DNA sequences
XX

SQ Sequence 243 BP; 74 A; 34 C; 33 G; 102 T; 0 U; 0 Other;

Query Match 100.0%; Score 243; DB 4; Length 243;
Best Local Similarity 100.0%; Pred. No. 1.8e-40;
Matches 243; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

QY 1 TCTGTTACAGGTCACCTAATACCCTAAGTAGTTCATAGTACGTCGATATGTTGTG 60
DB 1 TCTGTTACAGGTCACCTAATACCCTAAGTAGTTCATAGTACGTCGATATGTTGTG 60

QY 61 TTTTACAGTATTATAGTCTCTGTTTTATGCAAAATCTAATTTAATATATTGATATTTA 120
DB 61 TTTTACAGTATTATAGTCTCTGTTTTATGCAAAATCTAATTTAATATATTGATATTTA 120

QY 121 TATCATTTTACGTTTCTGTTTCAGCTTTTATACATAAGTTGGCATTATAAAAAAGCATT 180
DB 121 TATCATTTTACGTTTCTGTTTCAGCTTTTATACATAAGTTGGCATTATAAAAAAGCATT 180

QY 181 GCTTATCAATTTGTTGCAACGACAGGTCACCTATCAGTCMAAATAAATCATTTTGTAT 240
DB 181 GCTTATCAATTTGTTGCAACGACAGGTCACCTATCAGTCMAAATAAATCATTTTGTAT 240

QY 241 TTC 243
DB 241 TTC 243

```

RESULT 2

ACC85316
ID ACC85316 standard; DNA; 248 BP.

AC ACC85316;
AC

DT 18-SEP-2003 (first entry)

DE Recombinase lambda integrase attP DNA recognition sequence.

KW Vegetable plasmid transformation; transgenic; recognition sequence;
KW plant; site-specific integration; nutrition; seed production;
KW chemical production; ds.

OS Unidentified.

PN WO2003054201-A1.

PD 03-JUL-2003.

PF 16-DEC-2002; 2002WO-EP014303.

PR 20-DEC-2001; 2001DE-01063159.

PA (SUNG-) SUNGENE GMBH & CO KGAA.

PI Biesgen C;

DR WPI; 2003-541820/51.

PT Site-specific integration of DNA into plasmid DNA, useful for making
PT transgenic plants used e.g. as food, by recombinase-mediated insertion.

PS Disclosure; Page 35; 164pp; German.

CC The present invention relates to a method for the site-specific
CC integration of a DNA sequence into the plasmid DNA of a plant or its
CC derived cells. Transgenic plants in which a DNA sequence has been
CC integrated, also their cell cultures, organs, tissues etc. are useful in
CC human or animal nutrition, to produce seeds, and to produce
CC pharmaceuticals or fine chemicals, e.g. enzymes, vitamins, amino acids,
CC flavourings and aromatizing agents, dyes, antibodies and vaccines. The
CC present sequence is a recognition sequence shown in the exemplification
CC of the invention

SQ Sequence 248 BP; 76 A; 35 C; 34 G; 103 T; 0 U; 0 Other;

Query Match 100.0%; Score 243; DB 8; Length 248;
Best Local Similarity 100.0%; Pred. No. 1.8e-40;
Matches 243; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

QY 1 TCTGTTACAGGTCACCTAATACCCTAAGTAGTTCATAGTACGTCGATATGTTGTG 60
DB 1 TCTGTTACAGGTCACCTAATACCCTAAGTAGTTCATAGTACGTCGATATGTTGTG 60

QY 61 TTTTACAGTATTATAGTCTCTGTTTTATGCAAAATCTAATTTAATATATTGATATTTA 120
DB 61 TTTTACAGTATTATAGTCTCTGTTTTATGCAAAATCTAATTTAATATATTGATATTTA 120

QY 121 TATCATTTTACGTTTCTGTTTCAGCTTTTATACATAAGTTGGCATTATAAAAAAGCATT 180
DB 121 TATCATTTTACGTTTCTGTTTCAGCTTTTATACATAAGTTGGCATTATAAAAAAGCATT 180

QY 181 GCTTATCAATTTGTTGCAACGACAGGTCACCTATCAGTCMAAATAAATCATTTTGTAT 240
DB 181 GCTTATCAATTTGTTGCAACGACAGGTCACCTATCAGTCMAAATAAATCATTTTGTAT 240

QY 241 TTC 243
DB 241 TTC 243

```

RESULT 3

ACC44676
ID ACC44676 standard; DNA; 282 BP.

AC ACC44676;
AC

DT 29-MAY-2003 (first entry)

DE Murine rDNA PCR primer SEQ ID NO:72.

KW Chromosome-based platform; artificial chromosome; eukaryotic chromosome;
KW att site; integrase; recombinase; ACes; gene therapy; transgenic animal;
KW platform artificial chromosome expression system; gene; ds.

OS Mus musculus.

OS Synthetic.

PN WO200297059-A2.

PD 05-DEC-2002.

PF 30-MAY-2002; 2002WO-US017452.

PR 30-MAY-2001; 2001US-0294758P.

PR 21-MAR-2002; 2002US-0366891P.

PA (CHRO-) CHROMOS MOLECULAR SYSTEMS INC.

PI Perkins E, Perez C, Lindenbaum M, Greene A, Leung J, Fleming E;
PI Stewart S, Shellard J;

DR WPI; 2003-140461/13.

PT Novel eukaryotic chromosome comprising one or many att sites which
PT permits site-directed integration in the presence of lambda-integrase,
PT useful for site-specific recombination-directed integration of DNA of
PT interest.

PS Example 2; Page 207; 272pp; English.

CC The present invention describes a eukaryotic chromosome (I) comprising
CC one or several att sites, where an att site is heterologous to the
CC chromosome, and permits site-directed integration in the presence of
CC lambda-integrase. Also described: (i) a platform artificial chromosome
CC expression system (ACes) (ii) comprising several sites that participate
CC in recombinase catalysed recombination; and (2) a method (M1) for
CC introducing a heterologous nucleic acid into a platform artificial

CC chromosome. (I) can be used in gene therapy. (M1) is useful for
CC introducing a heterologous nucleic acid molecule into a platform
CC artificial chromosome, preferably an Aves. (II) is useful for producing a
CC transgenic animal (e.g. a fish, insect, reptile, amphibian, arachnid, or
CC mammal) by introducing (II) by cell fusion, lipid-mediated transfection,
CC by a carrier system, microinjection, microcell fusion, electroporation,
CC microprojectile bombardment or direct DNA transfer into an embryonic
CC cell, preferably a stem cell or an embryo. (II) comprises a heterologous
CC nucleic acid that encodes a therapeutic product which is useful for
CC making a library of Aves comprising random portions of a genome. ACC44612
CC to ACC44732 and ABP96650 to ABP96657 represent sequences used in the
CC exemplification of the present invention
XX
SQ Sequence 282 BP; 79 A; 49 C; 39 G; 115 T; 0 U; 0 Other;

Query Match 100.0%; Score 243; DB 7; Length 282;
Best Local Similarity 100.0%; Pred. No. 1.8e-40;
Matches 243; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCCTGTTACAGTCACTAATACCATCTAAGTAGTTGATTCATAGTGCATATGTTGTG 60
DB |||||
15 TCCTGTTACAGTCACTAATACCATCTAAGTAGTTGATTCATAGTGCATATGTTGTG 74
QY 61 TTTTACAGTATTAGTAGTCTGTTTTTATGCAAAATCTAATTAATATATTGATATTTA 120
DB |||||
75 TTTTACAGTATTAGTAGTCTGTTTTTATGCAAAATCTAATTAATATATTGATATTTA 134
QY 121 TATCATTTTACGTTCTCGTTACGCTTTTATGCAAAATCTAATTAATATATTGATATTTA 180
DB |||||
135 TATCATTTTACGTTCTCGTTACGCTTTTATGCAAAATCTAATTAATATATTGATATTTA 194
QY 181 GCTTATCAATTTGTTGCAACGACAGTCACTATCAGTCAAAATCTAATTAATATTTGAT 240
DB |||||
195 GCTTATCAATTTGTTGCAACGACAGTCACTATCAGTCAAAATCTAATTAATATTTGAT 254
QY 241 TTC 243
DB 255 TTC 257

RESULT 4
ABT16636
ID ABT16636 standard; DNA; 282 BP.
XX
AC ABT16636;
XX
XX 03-APR-2003 (first entry)
XX Artificial plant chromosome related oligo SEQ ID No 48.
XX
XX Plant artificial chromosome; PAC; transgenic plant; vaccine;
XX Blood factor; herbicide; stress; agronomical; nutrient quality;
XX bacterial artificial chromosome; BAC; yeast artificial chromosome; YAC;
XX ds.

OS Unidentified.
XX
XX W0200296923-Al.
XX
XX 05-DEC-2002.
XX
XX 30-MAY-2002; 2002WO-US017451.
XX
XX 30-MAY-2001; 2001US-0294687P.
XX 04-JUN-2001; 2001US-0296329P.
XX
XX (CHRO-) CHROMOS MOLECULAR SYSTEMS INC.
XX (AGRI-) AGRISOMA INC.
XX
XX Perez C, Fabijanski SF, Perkins E;
XX WPI; 2003-140436/13.
XX
XX

PT Producing artificial chromosome by introducing a nucleic acid into plant
PT cell, selecting artificial chromosome that has one or more repeat regions
XX with equivalent amounts of euchromatic and heterochromatic nucleic acids.
XX Disclosure; Page 263-264; 269pp; English.

CC The invention relates to a novel method for producing plant artificial
CC chromosomes. The invention also relates to methods for targeting
CC insertion of heterologous DNA into plant artificial chromosomes, methods
CC for delivery of plant chromosomes to selected cells and tissues. The
CC isolated plant artificial chromosome (PAC) is useful for producing a
CC transgenic plant, which involves introducing the PAC into a plant cell.
CC The PAC comprises a heterologous nucleic acid encoding a gene product.
CC such as enzymes, antisense RNA, rDNA, structural proteins, marker
CC proteins, ligands, receptors, ribozymes, therapeutic proteins, and
CC biopharmaceutical proteins, vaccines, blood factors, antigens, hormones,
CC cytokines, growth factors, antibodies, or a product that provides for
CC resistance to diseases, insects, herbicides, or stress in a plant. The
CC heterologous nucleic acid optionally encodes a product that provides an
CC agronomically important trait in the plant, e.g. a product that alters
CC nutrient use and/or improves the nutrient quality of the plant. The
CC heterologous nucleic acid is contained within a bacterial artificial
CC chromosome (BAC) or a yeast artificial chromosome (YAC). This
CC polynucleotide sequence represents an oligo relating to the method for
CC producing plant artificial chromosomes of the invention

SQ Sequence 282 BP; 79 A; 49 C; 39 G; 115 T; 0 U; 0 Other;

Query Match 100.0%; Score 243; DB 7; Length 282;
Best Local Similarity 100.0%; Pred. No. 1.8e-40;
Matches 243; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCCTGTTACAGTCACTAATACCATCTAAGTAGTTGATTCATAGTGCATATGTTGTG 60
DB |||||
15 TCCTGTTACAGTCACTAATACCATCTAAGTAGTTGATTCATAGTGCATATGTTGTG 74
QY 61 TTTTACAGTATTAGTAGTCTGTTTTTATGCAAAATCTAATTAATATATTGATATTTA 120
DB |||||
75 TTTTACAGTATTAGTAGTCTGTTTTTATGCAAAATCTAATTAATATATTGATATTTA 134
QY 121 TATCATTTTACGTTCTCGTTACGCTTTTATGCAAAATCTAATTAATATATTGATATTTA 180
DB |||||
135 TATCATTTTACGTTCTCGTTACGCTTTTATGCAAAATCTAATTAATATATTGATATTTA 194
QY 181 GCTTATCAATTTGTTGCAACGACAGTCACTATCAGTCAAAATCTAATTAATATTTGAT 240
DB |||||
195 GCTTATCAATTTGTTGCAACGACAGTCACTATCAGTCAAAATCTAATTAATATTTGAT 254
QY 241 TTC 243
DB 255 TTC 257

RESULT 5
AAF79770
ID AAF79770 standard; DNA; 610 BP.
XX
XX AAF79770;
XX
XX 29-MAY-2001 (first entry)
XX
XX Bacteriophage lambda attachment P region.
XX Attachment P region; attP; recombination; marker gene removal; ds.
XX Bacteriophage lambda.
XX
XX W0200121780-A2.
XX
XX 29-MAR-2001.
XX
XX 15-SEP-2000; 2000WO-GH003543.
XX

```

PR 17-SEP-1999; 99GB-00021937.
XX
XX (UYLE-) UNIV LEEDS.
XX
XX Meyer P, Zubko E;
XX
XX WPI; 2001-266072/27.
XX
XX Removing a part of a transgene which has been integrated into a genome
XX comprises inducing intrachromosomal homologous recombination between the
XX attachment P regions of bacteriophage lambda flanking the transgene.
XX
XX Claim 8; Fig 3D; 25pp; English.
XX
XX The present invention describes a method of removing a transgene marker
XX by flanking the transgene with a bacteriophage lambda attachment P (attP)
XX region and inducing homologous recombination between attP regions so that
XX the transgene is removed. This is useful in the production of transgenic
XX plants with less risk of inter-species transmission of marker genes
XX which often encode proteins associated with, for example, herbicide and
XX antibiotic resistance. The present sequence is the attP coding region
XX
XX Sequence 610 BP; 164 A; 108 C; 110 G; 228 T; 0 U; 0 Other;
XX
XX Query Match 100.0%; Score 243; DB 5; Length 610;
XX Best Local Similarity 100.0%; Pred. No. 1.9e-40;
XX Matches 243; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 1 TCTGTTACAGGTCACCTAATACCATCTAAGTAGTTCATGATGACATGATGTTG 60
XX Db 139 TCTGTTACAGGTCACCTAATACCATCTAAGTAGTTCATGATGACATGATGTTG 198
XX
XX 61 TTTTACAGTATTTATGATGCTCTGTTTTTATGCAAAATCTAATTTAATATTGATTTA 120
XX Db 139 TTTTACAGTATTTATGATGCTCTGTTTTTATGCAAAATCTAATTTAATATTGATTTA 258
XX
XX 121 TATCAATTTTACGTTTCTCGTTTCAGCTTTTATGCTAAGTTCGCAATTAATAAAGCATT 180
XX Db 259 TATCAATTTTACGTTTCTCGTTTCAGCTTTTATGCTAAGTTCGCAATTAATAAAGCATT 318
XX
XX 181 GCTTATCAATTTGTTGCAACGACAGGTCACCTATCAGTCAAAATAAATCATTATTGAT 240
XX Db 319 GCTTATCAATTTGTTGCAACGACAGGTCACCTATCAGTCAAAATAAATCATTATTGAT 378
XX
XX 241 TTC 243
XX Db 379 TTC 381
XX
XX RESULT 6
XX ID ABQ80306 standard; DNA; 1469 BP.
XX AC ABQ80306;
XX
XX 27-JUN-2003 (first entry)
XX
XX Lambda fragment in plasmid DNA.
XX
XX Primer; PCR; amplify; lambda phage; primer material; insertion; SNP;
XX deletion; single nucleotide polymorphism; sequencing; diagnosis; ss.
XX
XX Synthetic.
XX
XX WO2003027991-A1.
XX
XX 03-APR-2003.
XX
XX 24-SEP-2002; 2002WO-JP009766.
XX
XX 25-SEP-2001; 2001JP-00291249.
XX
XX (DNAF-) DNAFORM KK.
XX
PR (RIKE ) RIKEN KK.
XX
XX Hayashizaki Y;
XX
XX WPI; 2003-354676/33.
XX
XX Printed material useful as a delivery and storage system for oligomer
XX and/or polymer, comprises a support having an oligomer and/or polymer
XX applied on it.
XX
XX Example 1; Page 31-32; 91pp; English.
XX
XX The sequences given in ABQ80304-05 are primers which were used to amplify
XX DNA for use in the material of the invention. The primers amplify a 1377
XX bp portion of lambda phage DNA contained in a plasmid. The amplified
XX sequence (ABQ80306) was attached to the primer material of the invention
XX which comprises at least one support having at least one oligomer and/or
XX polymer applied on it. The printed material is useful in a method for
XX synthesising DNA where the product of amplification and/or ligation is
XX cDNA and/or full-length cDNA which is recovered and used for
XX determination of nucleotide insertion/deletion, single nucleotide
XX polymorphism (SNP) and sequencing analysis, in a diagnostic method for
XX determination of nucleotide insertion/deletion, or SNP analysis.
XX Optionally, the cDNA and/or full-length cDNA is useful for the peptide,
XX polypeptide or protein expression. The printed material is useful in
XX research applications, or for providing scientists with oligomer and/or
XX polymers from the printed materials easily and immediately. From the
XX printed material, at least an oligomer and/or polymer can be obtained
XX immediately and directly, without need to make a request for it. The
XX oligomers and/or polymers can be delivered and stored easily with reduced
XX labour and time while eliminating the need to use special equipment or
XX facilities. Thus, the printed material is a quick, efficient and
XX inexpensive sample delivery system
XX
XX Sequence 1469 BP; 411 A; 300 C; 280 G; 478 T; 0 U; 0 Other;
XX
XX Query Match 100.0%; Score 243; DB 7; Length 1469;
XX Best Local Similarity 100.0%; Pred. No. 1.9e-40;
XX Matches 243; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 1 TCTGTTACAGGTCACCTAATACCATCTAAGTAGTTCATGATGACATGATGTTG 60
XX Db 808 TCTGTTACAGGTCACCTAATACCATCTAAGTAGTTCATGATGACATGATGTTG 867
XX
XX 61 TTTTACAGTATTTATGATGCTCTGTTTTTATGCAAAATCTAATTTAATATTGATTTA 120
XX Db 868 TTTTACAGTATTTATGATGCTCTGTTTTTATGCAAAATCTAATTTAATATTGATTTA 927
XX
XX 121 TATCAATTTTACGTTTCTCGTTTCAGCTTTTATGCTAAGTTCGCAATTAATAAAGCATT 180
XX Db 928 TATCAATTTTACGTTTCTCGTTTCAGCTTTTATGCTAAGTTCGCAATTAATAAAGCATT 987
XX
XX 181 GCTTATCAATTTGTTGCAACGACAGGTCACCTATCAGTCAAAATAAATCATTATTGAT 240
XX Db 988 GCTTATCAATTTGTTGCAACGACAGGTCACCTATCAGTCAAAATAAATCATTATTGAT 1047
XX
XX 241 TTC 243
XX Db 1048 TTC 1050
XX
XX RESULT 7
XX ACC83020
XX ID ACC83020 standard; DNA; 1469 BP.
XX AC ACC83020;
XX
XX 27-AUG-2003 (first entry)
XX
XX Bacteriophage lambda DNA, SEQ ID NO:3 used in the invention.
XX
XX Oligomer storage; oligomer delivery; ds.
XX

```

OS Bacteriophage lambda.
 XX W02003040360-A1.
 XX
 XX PD 15-MAY-2003.
 XX
 XX PF 05-NOV-2002; 2002WO-JF011492.
 XX
 XX PR 05-NOV-2001; 2001JP-00339217.
 XX
 XX PA (RIKE) RIKEN KK.
 XX PA (DNAF-) DNAFORM KK.
 XX PA (HAYA/) HAYASHIZAKI Y.
 XX
 XX PI Hayashizaki Y;
 XX
 XX DR WPI; 2003-441569/41.
 XX
 XX PT New support useful for storing and/or delivering an oligomer and/or
 PT polymer applied on support, has oligomer and/or polymer applied on it,
 PT and a loose-leaf sheet or a card.
 XX
 XX PS Example 1; Page 30-31; 70pp; English.
 XX
 XX CC The invention relates to a method for storing and/or delivering an
 CC oligomer and/or polymer applied on support. The support has oligomer
 CC and/or polymer applied on it, and is in the form of loose-leaf sheet or a
 CC card. The support is useful for storing and/or delivering an oligomer
 CC and/or polymer applied on it. The present sequence is Bacteriophage
 CC lambda DNA used in the exemplification of the invention
 XX
 XX SQ Sequence 1469 BP; 411 A; 300 C; 280 G; 478 T; 0 U; 0 Other;
 SQ
 Query Match 100.0%; Score 243; DB 7; Length 1469;
 Best Local Similarity 100.0%; Pred. No. 1.9e-40;
 Matches 243; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 TCTGTTACAGGTCACCTAATACCATCTAAGTAGTGTGATTCATAGTACGATGATGTTGTG 60
 Db 808 TCTGTTACAGGTCACCTAATACCATCTAAGTAGTGTGATTCATAGTACGATGATGTTGTG 867
 QY 61 TTTTACAGTATTATGATGCTGTTTTTATGCAAAATCTAATTAATATATATGATATTTA 120
 Db 868 TTTTACAGTATTATGATGCTGTTTTTATGCAAAATCTAATTAATATATATGATATTTA 927
 QY 121 TATCATTTTACGTTTCTCGTTTCAGCTTTTATTAATTAAGTTGGCATTATATAAAGCATT 180
 Db 928 TATCATTTTACGTTTCTCGTTTCAGCTTTTATTAATTAAGTTGGCATTATATAAAGCATT 987
 QY 181 GCTTATCAATTTGTTGCAACGACGATCCTATCATGTCATCAAAATATAAATCATTTTGTAT 240
 Db 988 GCTTATCAATTTGTTGCAACGACGATCCTATCATGTCATCAAAATATAAATCATTTTGTAT 1047
 QY 241 TTC 243
 Db 1048 TTC 1050
 RESULT 8
 AAZ30709/c
 ID AAZ30709 standard; cDNA; 1763 BP.
 XX
 XX AC AAZ30709;
 XX
 XX DT 05-JAN-2000 (first entry)
 XX
 XX DE Rat neuronal immediate early gene cDNA clone R280.
 XX
 XX KW Immediate early gene; IEG; neuron; brain; function; growth factor;
 KW transcription factor; signal transduction; cytoskeletal protein;
 KW metabolic enzyme; learning; memory; synaptic transmission; tolerance;
 KW neuronal plasticity; ds.
 XX

OS Rattus sp.
 XX
 XX FN W09940225-A1.
 XX
 XX PD 12-AUG-1999.
 XX
 XX PF 05-FEB-1999; 99WO-US002462.
 XX
 XX PR 09-FEB-1998; 98US-0074135P.
 XX PR 12-FEB-1998; 98US-0074518P.
 XX
 XX PA (UWJO) UNIV JOHNS HOPKINS SCHOOL MEDICINE.
 XX PA (BADI) BASF-LYNX BIOSCIENCE AG.
 XX
 XX PI Worley PF, Lanahan A, Goetz B, Hiemisch H, Kuner R, Scheek S;
 XX PI Nikolich K, Zhukovski E;
 XX
 XX DR WPI; 1999-590697/50.
 XX
 XX PT Novel genes and polypeptides, useful for treating conditions related to a
 PT deficiency in nIEG responsiveness to a stimulus.
 XX
 XX PS Claim 1; Page 114-115; 134pp; English.
 XX
 XX CC This sequence represents rat neuronal immediate early gene (IEG) cDNA
 CC clone R280. An IEG is a gene whose expression is rapidly increased
 CC immediately following a stimulus e.g., neuronal stimulation. Such
 CC neuronal IEGs have been found to encode a variety of proteins, including
 CC transcription factors, cytoskeletal proteins, growth factors and
 CC metabolic enzymes, as well as proteins involved in signal transduction.
 CC The identification of neuronal IEGs and the proteins they encode may
 CC provide important information about the function of neurons in, for
 CC example, learning, memory, synaptic transmission, tolerance and neuronal
 CC plasticity. Neuronal IEGs, neuronal IEG protein products, cells
 CC expressing neuronal IEGs and antibodies against neuronal IEG proteins can
 CC be used to treat an animal with a deficiency in neuronal IEG responsivity
 CC to stimuli, such that the effect of the deficiency is minimised. The
 CC deficiency may be a reduced or elevated level of expression of an IEG.
 CC The neuronal stimulus comprises a maximal electroconvulsive seizure and
 CC its effects influence learning or memory. The IEGs and protein products
 CC are useful in identifying compounds that modulate the expression or
 CC activity of IEG nucleic acids or proteins, respectively
 XX
 XX SQ Sequence 1763 BP; 478 A; 402 C; 452 G; 424 T; 0 U; 7 Other;
 SQ
 Query Match 100.0%; Score 243; DB 2; Length 1763;
 Best Local Similarity 100.0%; Pred. No. 1.9e-40;
 Matches 243; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 TCTGTTACAGGTCACCTAATACCATCTAAGTAGTGTGATTCATAGTACGATGATGTTGTG 60
 Db 431 TCTGTTACAGGTCACCTAATACCATCTAAGTAGTGTGATTCATAGTACGATGATGTTGTG 372
 QY 61 TTTTACAGTATTATGATGCTGTTTTTATGCAAAATCTAATTAATATATATGATATTTA 120
 Db 371 TTTTACAGTATTATGATGCTGTTTTTATGCAAAATCTAATTAATATATATGATATTTA 312
 QY 121 TATCATTTTACGTTTCTCGTTTCAGCTTTTATTAATTAAGTTGGCATTATATAAAGCATT 180
 Db 311 TATCATTTTACGTTTCTCGTTTCAGCTTTTATTAATTAAGTTGGCATTATATAAAGCATT 252
 QY 181 GCTTATCAATTTGTTGCAACGACGATCCTATCATGTCATCAAAATATAAATCATTTTGTAT 240
 Db 251 GCTTATCAATTTGTTGCAACGACGATCCTATCATGTCATCAAAATATAAATCATTTTGTAT 192
 QY 241 TTC 243
 Db 191 TTC 189
 RESULT 9
 ACC44716
 ID ACC44716 standard; DNA; 4346 BP.

Best Local Similarity 100.0%; Pred. No. 1.9e-40;
Matches 243; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCTGTTACAGTCACTAATACCACTAAGTAGTTGATTCATAGTGCATATGTTGTG 60
Db 4070 TCTGTTACAGTCACTAATACCACTAAGTAGTTGATTCATAGTGCATATGTTGTG 4129

QY 61 TTTTACAGTATTATGATGCTGTTTTTATGCAAACTAATTTAATATATGATATTTA 120
Db 4130 TTTTACAGTATTATGATGCTGTTTTTATGCAAACTAATTTAATATATGATATTTA 4189

QY 121 TATCATTTTACGTTTCGTTTCAGCTTTTATATGCAAACTAATTTAATATATGATATTTA 180
Db 4190 TATCATTTTACGTTTCGTTTCAGCTTTTATATGCAAACTAATTTAATATATGATATTTA 4249

QY 181 GCTTATCAATTTGTTGCAACAGAGTCACTATCAGTCAAAATAAATCAATATTTGAT 240
Db 4250 GCTTATCAATTTGTTGCAACAGAGTCACTATCAGTCAAAATAAATCAATATTTGAT 4309

QY 241 TTC 243
Db 4310 TTC 4312

RESULT 11
AAT18924/c
ID AAT18924 standard; DNA; 4909 BP.

XX AC AAT18924;
XX 17-JAN-1997 (first entry)
XX Plasmid pA126i.

KW Spider; dragline protein; variant; monomer; polymer; circular;
KW fibre forming region; Spidroin 1; Nephila clavipes; Dp1; mimic;
KW DP-1A analogue; fibre; high tensile strength; elasticity; clothing; rope;
KW surgical suture; implant; reinforcement; film; coating; ss.
XX Synthetic.
OS
FN WO9429450-A2.
XX 22-DEC-1994.
XX 15-JUN-1994; 94WO-US006689.
XX 15-JUN-1993; 93US-00077600.
XX (DUPO) DU PONT DE NEMOURS & CO E I.
XX Fahnstock SR;
XX WP1; 1995-036479/05.
XX New synthetic variants of spider dragline protein - for making fibres
XX useful as clothing, surgical silk, plastic reinforcement etc., also
XX related DNA, vectors and transformed cells.
XX Example 1; Fig 13; 168pp; English.

CC This sequence represents the complete nucleotide sequence of the plasmid
CC pA126i. This plasmid was used in the construction of the vector pPF510
CC which was used to express synthetic spider dragline variants, DP-1A.9 and
CC DP-1B.9. pA126i comprises a replication origin active in E. coli, a
CC selectable genetic marker which is a gene conferring resistance to
CC ampicillin, sites for the restriction endonucleases BamHI and BglII with
CC no essential sequences between them, and a third restriction site for
CC PstI, located within the selectable marker which produces cohesive ends
CC incompatible with those produced by BamHI and BglII. The polypeptide
CC monomers are variants based on a consensus sequence derived from the
CC fibre forming regions of spider dragline protein, esp. the natural
CC protein 1 (Spidroin 1) from Nephila clavipes. Synthetic analogues of Dp1

CC were designed to mimic the repeating consensus sequence of the natural
CC protein and the pattern of variation among individual repeats. DP-1A
CC analogues are composed of a tandemly repeated 101 amino acid monomer
CC which comprises four repeats which differ from the consensus sequence
CC given in AAW06201, according to the pattern (1)-(5): (1) the poly-alanine
CC sequence varies in length from 0-7 residues; (2) when the entire poly-
CC alanine sequence is deleted, so also is the surrounding sequence
CC encompassing AGGGGGGGAGANGG; (3) aside from the poly-alanine sequence,
CC deletions usually encompass integral multiples of three consecutive
CC residues; (4) deletion of GYG is generally accompanied by deletion of GRG
CC in the same sequence; and (5) a repeat in which the entire poly-alanine
CC sequence is deleted is generally preceded by a repeat containing six
CC alanine residues. The proteins may be used to produce fibres of high
CC tensile strength and elasticity, suitable for clothing, rope, surgical
CC sutures, biomaterials for implants, plastic reinforcements, films,
CC coatings, etc
XX
SQ Sequence 4909 BP; 1216 A; 1251 C; 1258 G; 1184 T; 0 U; 0 Other;

Query Match 100.0%; Score 243; DB 2; Length 4909;
Best Local Similarity 100.0%; Pred. No. 1.9e-40;
Matches 243; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCTGTTACAGTCACTAATACCACTAAGTAGTTGATTCATAGTGCATATGTTGTG 60
Db 2516 TCTGTTACAGTCACTAATACCACTAAGTAGTTGATTCATAGTGCATATGTTGTG 2457

QY 61 TTTTACAGTATTATGATGCTGTTTTTATGCAAACTAATTTAATATATGATATTTA 120
Db 2456 TTTTACAGTATTATGATGCTGTTTTTATGCAAACTAATTTAATATATGATATTTA 2397

QY 121 TATCATTTTACGTTTCGTTTCAGCTTTTATATGCAAACTAATTTAATATATGATATTTA 180
Db 2396 TATCATTTTACGTTTCGTTTCAGCTTTTATATGCAAACTAATTTAATATATGATATTTA 2337

QY 181 GCTTATCAATTTGTTGCAACAGAGTCACTATCAGTCAAAATAAATCAATATTTGAT 240
Db 2336 GCTTATCAATTTGTTGCAACAGAGTCACTATCAGTCAAAATAAATCAATATTTGAT 2277

QY 241 TTC 243
Db 2276 TTC 2274

RESULT 12
AAF30800
ID AAF30800 standard; DNA; 5641 BP.

XX AC AAF30800;
XX 11-SEP-2003 (revised)
XX 21-JUN-2001 (first entry)
XX Vector plasmid pJMF3 encoding LacZ-chitinase fusion.
XX Chitinase; reporter gene; LacZ gene; promoter; vector; pJMF3; ds.
XX Escherichia coli.
XX Vibrio harveyi.
XX Bacteriophage lambda.
XX Chimeric.

XX Key Location/Qualifiers
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FT /*note= "CAP-cAMP binding site"
FT -35_signal 1820..1826
FT /*tag= b
FT /*function= "Lac promoter"
FT -10_signal 1845..1850
FT /*tag= c
FT /*function= "Lac promoter"
FT protein_bind 1857..1883

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FT      /*tag= d
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FT      1895..2014
FT      /*tag= e
FT      /partial
FT      /product= "lacZ-chitobiase fusion"
XX
XX      WO200127322-A2.
XX
XX      19-APR-2001.
XX
XX      02-AUG-2000; 2000WO-US021048.
XX
XX      13-OCT-1999; 99US-0159221P.
XX
XX      (ELIT-) ELITRA PHARM INC.
XX
XX      Zyskind J;
XX
XX      WPI; 2001-290731/30.
XX      P-PSDB; AAB20484.
XX
XX      Identifying a regulatory element capable of directing or regulating
XX      transcription (e.g. a promoter) comprises providing a construct linked to
XX      a nucleic acid encoding a cytoplasmic form of chitobiase.
XX
XX      Example 1; Page 32-34; 44pp; English.
XX
XX      The present sequence is that of vector plasmid pJMF3, which includes
XX      phage lambda attP and the lac promoter with the first 21 amino acids of
XX      lacZ-alpha (from plasmid pUC19) fused in-frame to the Vibrio harveyi
XX      chitobiase gene (see AAB20484). The invention relates to genetic
XX      constructs and methods of using a cytoplasmic form of chitobiase enzyme
XX      as a reporter. A claimed reporter gene construct comprises pJMF3. The
XX      invention also comprises expression vectors which express the cytoplasmic
XX      form of chitobiase. Methods are provided for: characterizing a promoter;
XX      identifying a regulatory element capable of directing and regulating
XX      transcription within a test sequence; detecting a successful
XX      transformation; and for monitoring the activity of a promoter. Chitobiase
XX      has an advantage over beta-galactosidase as a reporter gene in that it is
XX      not necessary to engineer many host cells to lack reporter activity.
XX      (Updated on 11-SEP-2003 to standardise OS field)
XX
XX      Sequence 5641 BP; 1539 A; 1305 C; 1336 G; 1461 T; 0 U; 0 Other;
XX
XX      Query Match      100.0%; Score 243; DB 4; Length 5641;
XX      Best Local Similarity 100.0%; Pred. No. 1.9e-40;
XX      Matches 243; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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XX      4703      TCTGTTACAGGTCACCTAAATACCACCTAAGTACTGATTCATAGTGCATCATGTTG 4762
XX
XX      QY      61      TTTTACAGTATTATGATGCTGTTTTTTATGCAAAATCTAATTTAATATATTGATTTA 120
XX      Db      |||||
XX      4763      TTTTACAGTATTATGATGCTGTTTTTTATGCAAAATCTAATTTAATATATTGATTTA 4822
XX
XX      QY      121      TATCATTTTACGTTTCTCGTTCAGCTTTTATATACCTAAGTGGCATTATAAAAGCATT 180
XX      Db      |||||
XX      4823      TATCATTTTACGTTTCTCGTTCAGCTTTTATATACCTAAGTGGCATTATAAAAGCATT 4882
XX
XX      QY      181      GCTTATCAATTTGTTGCAAGACAGTCAGTCACTATCAATCAAAATAAATCAATTTTGAT 240
XX      Db      |||||
XX      4883      GCTTATCAATTTGTTGCAAGACAGTCAGTCACTATCAATCAAAATAAATCAATTTTGAT 4942
XX
XX      QY      241      TTC 243
XX      Db      |||
XX      4943      TTC 4945
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XX      RESULT 13
XX      AAF30801/c
XX      ID      AAF30801 standard; DNA; 5670 BP.

```

```

XX      AAF30801;
XX
XX      11-SEP-2003 (revised)
XX      21-JUN-2001 (first entry)
XX
XX      Vector plasmid pJMF4 encoding LacZ-chitobiase fusion.
XX
XX      Chitobiase; reporter gene; LacZ gene; promoter; vector; pJMF4; ds.
XX
XX      Escherichia coli.
XX      Vibrio harveyi.
XX      Bacteriophage lambda.
XX      Chimeric.
XX
XX      Key      Location/Qualifiers
XX      protein_bind      1783..1810
XX      FT      /*tag= a
XX      FT      /note= "CAP-cAMP binding site"
XX      FT      1820..1826
XX      FT      /*tag= b
XX      FT      /function= "Lac promoter"
XX      FT      1845..1850
XX      FT      /*tag= c
XX      FT      /function= "Lac promoter"
XX      FT      1857..1883
XX      FT      /*tag= d
XX      FT      /note= "Lac repressor binding site"
XX      FT      1895..2014
XX      FT      /*tag= e
XX      FT      /partial
XX      FT      /product= "lacZ-chitobiase fusion"
XX
XX      WO200127322-A2.
XX
XX      19-APR-2001.
XX
XX      02-AUG-2000; 2000WO-US021048.
XX
XX      13-OCT-1999; 99US-0159221P.
XX
XX      (ELIT-) ELITRA PHARM INC.
XX
XX      Zyskind J;
XX
XX      WPI; 2001-290731/30.
XX      P-PSDB; AAB20484.
XX
XX      Identifying a regulatory element capable of directing or regulating
XX      transcription (e.g. a promoter) comprises providing a construct linked to
XX      a nucleic acid encoding a cytoplasmic form of chitobiase.
XX
XX      Example 1; Page 34-36; 44pp; English.
XX
XX      The present sequence is that of vector plasmid pJMF4, which includes
XX      phage lambda attP and the lac promoter with the first 21 amino acids of
XX      lacZ-alpha (from plasmid pUC19) fused in-frame to the Vibrio harveyi
XX      chitobiase gene (see AAB20484). The invention relates to genetic
XX      constructs and methods of using a cytoplasmic form of chitobiase enzyme
XX      as a reporter. A claimed reporter gene construct comprises pJMF4. The
XX      invention also comprises expression vectors which express the cytoplasmic
XX      form of chitobiase. Methods are provided for: characterizing a promoter;
XX      identifying a regulatory element capable of directing and regulating
XX      transcription within a test sequence; detecting a successful
XX      transformation; and for monitoring the activity of a promoter. Chitobiase
XX      has an advantage over beta-galactosidase as a reporter gene in that it is
XX      not necessary to engineer many host cells to lack reporter activity.
XX      (Updated on 11-SEP-2003 to standardise OS field)
XX
XX      Sequence 5670 BP; 1567 A; 1302 C; 1356 G; 1445 T; 0 U; 0 Other;
XX
XX      Query Match      100.0%; Score 243; DB 4; Length 5670;
XX      Best Local Similarity 100.0%; Pred. No. 1.9e-40;

```


CC The present sequence is that of vector plasmid pDYK11, which comprises
CC the Vibrio harveyi chitinase gene under the control of the Escherichia
CC coli rpmH-dnaA promoter in plasmid pACYC184. The plasmid encodes a dnaA-
CC chitinase fusion protein (see AAB20485). It was used to assess the
CC regulation of the dnaA gene using chitinase as a reporter enzyme. A
CC claimed reporter gene construct comprises pDYK11. The invention relates
CC to genetic constructs and methods of using a cytoplasmic form of
CC chitinase enzyme as a reporter. The invention also comprises expression
CC vectors which express the cytoplasmic form of chitinase. Methods are
CC provided for: characterizing a promoter; identifying a regulatory element
CC capable of directing and regulating transcription within a test sequence;
CC detecting a successful transformation; and for monitoring the activity of
CC a promoter. Chitinase has an advantage over beta-galactosidase as a
CC reporter gene in that it is not necessary to engineer many host cells to
CC lack reporter activity. (Updated on 11-SEP-2003 to standardise OS field)

XX
SQ Sequence 6071 BP; 1638 A; 1400 C; 1451 G; 1582 T; 0 U; 0 Other;
Query Match 100.0%; Score 243; DB 4; Length 6071;
Best Local Similarity 100.0%; Pred. No. 1.9e-40;
Matches 243; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TCTGTTACAGGTCACATAACCATCTAAGTAGTTCGATTCATAGTCACTGCATATGTTGG 60
Db 5133 TCTGTTACAGGTCACATAACCATCTAAGTAGTTCGATTCATAGTCACTGCATATGTTGG 5192
QY 61 TTTTACAGTATTATGATGCTCTGTTTTTATGCAAAATCTAATTTAATATATTGATATTA 120
Db 5193 TTTTACAGTATTATGATGCTCTGTTTTTATGCAAAATCTAATTTAATATATTGATATTA 5252
QY 121 TATCATTTTACGTTTCTCGTTTCAGCTTTTTTATCTAAGTTGGCATTTAAAAAGCATT 180
Db 5253 TATCATTTTACGTTTCTCGTTTCAGCTTTTTTATCTAAGTTGGCATTTAAAAAGCATT 5312
QY 181 GCTTATCAATTTGTTGCAACGAGGTCATCATCAGTCAAAATATAAATCATTTATTGAT 240
Db 5313 GCTTATCAATTTGTTGCAACGAGGTCATCATCAGTCAAAATATAAATCATTTATTGAT 5372
QY 241 TTC 243
Db 5373 TTC 5375

Search completed: September 9, 2004, 18:05:39
Job time : 277.724 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: September 9, 2004, 17:30:16 : Search time 1962.91 Seconds
(without alignments)
3696.811 Million cell updates/sec

Title: US-10-082-772B-2

Perfect score: 243

Sequence: 1 tctgtacaggtcactaata.....taaaatcattattgatttc 243

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 27513289 seqs, 14931090276 residues

Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST:*

- 1: em_estba:*
- 2: em_esthum:*
- 3: em_estin:*
- 4: em_estmu:*
- 5: em_estov:*
- 6: em_estpl:*
- 7: em_estro:*
- 8: em_htc:*
- 9: gb_est1:*
- 10: gb_est2:*
- 11: gb_htc:*
- 12: gb_est3:*
- 13: gb_est4:*
- 14: gb_est5:*
- 15: em_estfun:*
- 16: em_eston:*
- 17: em_gss_hum:*
- 18: em_gss_inv:*
- 19: em_gss_pln:*
- 20: em_gss_vrt:*
- 21: em_gss_fun:*
- 22: em_gss_mam:*
- 23: em_gss_mus:*
- 24: em_gss_pro:*
- 25: em_gss_rod:*
- 26: em_gss_phg:*
- 27: em_gss_vrl:*
- 28: gb_gss1:*
- 29: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
C 1	243	100.0	712	28	AQ990809	AQ990809 Rfc01638
C 2	214.8	88.4	395	28	AQ991303	AQ991303 Rfc02205
C 3	211.4	87.0	769	28	AQ990470	AQ990470 Rfc01245
C 4	208.8	85.9	764	28	AQ990878	AQ990878 Rfc01715

C 5	197	81.1	472	13	BQ157398	BQ157398 NF104D071
C 6	197	81.1	473	13	BQ156404	BQ156404 NF092E031
C 7	187.4	77.1	751	28	AQ989566	AQ989566 Rfc00126
C 8	186.4	76.7	743	28	AQ990346	AQ990346 Rfc01106
C 9	185.6	76.4	299	13	BY115594	BY115594 BY115594
C 10	175.2	72.1	753	28	AQ990861	AQ990861 Rfc01698
C 11	165.8	68.2	746	28	AQ990173	AQ990173 Rfc00898
C 12	160.8	66.2	770	28	AQ991774	AQ991774 Rfc02039F
C 13	160.8	66.2	791	28	AQ991791	AQ991791 Rfc02368F
C 14	159.4	65.6	695	28	AQ991039	AQ991039 Rfc01894
C 15	159	65.4	719	28	AQ991352	AQ991352 Rfc02270
C 16	157.2	64.7	767	28	AQ990301	AQ990301 Rfc01055
C 17	156.2	64.3	708	28	AQ990869	AQ990869 Rfc01706
C 18	155.4	64.0	827	14	CF347641	CF347641 AGENCOURT
C 19	152.8	62.9	755	14	CF347718	CF347718 AGENCOURT
C 20	150.2	61.8	787	14	CF347604	CF347604 AGENCOURT
C 21	150	61.7	597	12	BI422679	BI422679 EST533345
C 22	149	61.3	808	28	AQ990388	AQ990388 Rfc01153
C 23	144	59.3	206	13	BQ156416	BQ156416 NF092F021
C 24	140	57.6	777	14	CF347686	CF347686 AGENCOURT
C 25	139.6	57.4	756	28	AQ991732	AQ991732 Rfc00380F
C 26	135.2	55.6	715	28	AQ991358	AQ991358 Rfc02278
C 27	134.6	55.4	583	14	CB403882	CB403882 OSTR013H1
C 28	132.4	54.5	764	28	AQ990110	AQ990110 Rfc00827
C 29	129.8	53.4	393	14	CB403984	CB403984 OSTR015E7
C 30	128	52.7	664	28	AQ991011	AQ991011 Rfc01864
C 31	123.6	50.9	487	14	CB395230	CB395230 OSTR151B2
C 32	122.2	50.3	675	28	AQ991241	AQ991241 Rfc02132
C 33	121	49.8	556	28	AQ991338	AQ991338 Rfc02255
C 34	114.2	47.0	758	28	AQ991690	AQ991690 Rfc01924F
C 35	107	44.0	672	28	AQ990864	AQ990864 Rfc01701
C 36	102.8	42.3	553	14	CF347596	CF347596 AGENCOURT
C 37	100.4	41.3	360	9	AU244794	AU244794 AU244794
C 38	100.4	41.3	417	12	BM134283	BM134283 WHE0488.B
C 39	92.4	38.0	262	14	CB395877	CB395877 OSTR163A3
C 40	92.2	37.9	811	14	CF347776	CF347776 AGENCOURT
C 41	91.6	37.7	622	10	BE45088	BE45088 EST406166
C 42	90.8	37.4	227	14	CB398923	CB398923 OSTR212B6
C 43	90.8	37.4	263	14	CB395890	CB395890 OSTR163C2
C 44	90.6	37.3	247	14	CB401020	CB401020 OSTF186E2
C 45	89.6	36.9	381	13	BX508371	BX508371 DKFP686D

ALIGNMENTS

RESULT 1
AQ990809/c
LOCUS AQ990809 712 bp DNA linear GSS 14-AUG-2000
DEFINITION Rfc01638 Photorhabdus luminescens strain W14 M13 library
Photorhabdus luminescens genomic clone PLG01638, genomic survey
sequence.

ACCESSION AQ990809
VERSION AQ990809.1 GI:9649403

KEYWORDS GSS.

SOURCE Photorhabdus luminescens

ORGANISM Photorhabdus luminescens

REFERENCE Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;

Enterobacteriaceae; Photorhabdus.

1 (bases 1 to 712)

french-Constant,R.H., Waterfield,N., Burland,V., Perna,N.T.,

Daborn,P.J., Bowen,D. and Blatner,F.R.

A genomic sample sequence of the entomopathogenic bacterium

Photorhabdus luminescens W14: potential implications for virulence

Appl. Environ. Microbiol. 66 (8), 3310-3329 (2000)

JOURNAL 20378633

MEDLINE 10919786

PUBMED

COMMENT

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University of Bath

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Tel: (44) 1225 826621

Fax: (44) 1225 826779

Email: bsrfc@bath.ac.uk
This is one of 2,122 random reads from the M13 library. For annotation of identified clones (BLASTX, BLASTN and mapping to E. coli K12 genome) please see french-Constant et al. 2000, Nucleic Acids Res.
Seq primer: M13 Forward
Class: shotgun.
Location/Qualifiers
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/organism="Photorhabdus luminescens"
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Best Local Similarity 100.0%; Pred. No. 2.6e-36;
Matches 243; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TCTGTTACAGGTCACCTAAATACCATCTAAGTAGTGTGATTCATAGTGCATCATATGTTG 60
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DB 471 TATCAATTTACGTTCTCGTTCAGCTTTTATPACTAAGTGGCATATATAAAAGCATT 412
QY 181 GCTATCAATTTGTTCAACGACAGTCATCATCTAGTCAAAATAAATCAATTTTGTAT 240
DB 411 GCTATCAATTTGTTGCAACGACAGTCATCATCTAGTCAAAATAAATCAATTTTGTAT 352
QY 241 TTC 243
DB 351 TTC 349

RESULT 2
AQ991303/c
LOCUS
DEFINITION
Photorhabdus luminescens genomic clone PLG02205, genomic survey sequence.
ACCESSION
AQ991303
VERSION
AQ991303.1 GI:9649897
KEYWORDS
GSS.
SOURCE
Photorhabdus luminescens
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales; Enterobacteriaceae; Photorhabdus.
REFERENCE
1 (bases 1 to 395)
french-Constant,R.H., Waterfield,N., Burland,V., Perna,N.T., Daborn,P.J., Bowen,D. and Blattner,F.R.
A genomic sample sequence of the entomopathogenic bacterium Photorhabdus luminescens W14: potential implications for virulence Appl. Environ. Microbiol. 66 (8), 3310-3329 (2000)
JOURNAL
MEDLINE
20378633
PUBMED
10919786
COMMENT
Contact: french-Constant RH
Department of Biology and Biochemistry
University of Bath
South Building, Bath BA2 7AY, UK
Tel: (44) 1225 826621
Fax: (44) 1225 826779

Email: bsrfc@bath.ac.uk
This is one of 2,122 random reads from the M13 library. For annotation of identified clones (BLASTX, BLASTN and mapping to E. coli K12 genome) please see french-Constant et al. 2000, Nucleic Acids Res.
Seq primer: M13 Forward
Class: shotgun.
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/note="Genomic DNA from strain W14 was size selected (1-2 kb) and then cloned into M13 Janus."

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Best Local Similarity 94.2%; Pred. No. 6.1e-31;
Matches 227; Conservative 0; Mismatches 13; Indels 1; Gaps 1;
QY 3 TGTTCAGGTCACCTAATACCATCTAAGTAGTGTGATTCATAGTGCATATGTTGTT 62
DB 345 TGTTCAGGTCACCTAATACCATCTAAGTAGTGTGATTCATAGTGCATATGTTGTT 287
QY 63 TTACAGTATTATGATGCTGTTTTTATGCAAAATCTAATTAATATATGATATTATA 122
DB 286 TTACAGTATTATGATGCTGTTTTTATGCAAAATCTAATTAATATATGATATTATA 227
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DB 226 TCATTTTACGTTCTCGTTCAGCTTTTATATCTAGTTGGCATTTATAAAAGCATTC 167
QY 183 TTATCAATTTGTTGCAACGACAGTCATCTAGTCAAAATAAATCAATTTTGTATTT 242
DB 166 TTATCAATTTGTTGCAACGACAGTCATCTAGTCAAAATAAATCAATTTTGTATTT 107
QY 243 C 243
DB 106 C 106

RESULT 3
AQ990470/c
LOCUS
DEFINITION
Photorhabdus luminescens genomic clone PLG01245, genomic survey sequence.
ACCESSION
AQ990470
VERSION
AQ990470.1 GI:9649064
KEYWORDS
GSS.
SOURCE
Photorhabdus luminescens
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales; Enterobacteriaceae; Photorhabdus.
REFERENCE
1 (bases 1 to 769)
french-Constant,R.H., Waterfield,N., Burland,V., Perna,N.T., Daborn,P.J., Bowen,D. and Blattner,F.R.
A genomic sample sequence of the entomopathogenic bacterium Photorhabdus luminescens W14: potential implications for virulence Appl. Environ. Microbiol. 66 (8), 3310-3329 (2000)
JOURNAL
MEDLINE
20378633
PUBMED
10919786
COMMENT
Contact: french-Constant RH
Department of Biology and Biochemistry
University of Bath
South Building, Bath BA2 7AY, UK
Tel: (44) 1225 826621
Fax: (44) 1225 826779

Email: bsrfc@bath.ac.uk

This is one of 2,122 random reads from the M13 library. For annotation of identified clones (BLASTX, BLASTN and mapping to E. coli K12 genome) please see ffrench-Constant et al. 2000, Nucleic Acids Res.

Seq primer: M13 Forward

Class: shotgun.

FEATURES
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Location/Qualifiers
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/mol_type="genomic DNA"
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/db_xref="taxon:29488"
/clone="PLG01245"
/dev_stage="primary phase variant"
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/note="Genomic DNA from strain W14 was size selected (1-2 kb) and then cloned into M13 Janus."

ORIGIN

Query Match 87.0%; Score 211.4; DB 28; Length 769;
Best Local Similarity 94.2%; Pred. No. 2.1e-30;
Matches 229; Conservative 0; Mismatches 13; Indels 1; Gaps 1;
QY 2 CTGTTCAGGTCACATAACCATCTAAGTAGTTCATTCATAGTGCATATGTTGTT 61
Db 769 CTGTTCAGGTCACATCCCATTTAAAGTAGTTCATTCATAGTGCATATGTTGTT 710
QY 62 TTTACAGTATATCTAGTCTCTGTTTTTATGCAAAATCTAAATTAATATATGATTTAT 121
Db 709 TTNACAGTATATCTAGTCTCTGTTTTTATGCAAAATCTAAATTAATATATGATTTAT 650
QY 122 ATCATTTTACGTTTC-TGGTTCAGCTTTTATATCTAAGTGGCATTAATAAAGCAATT 180
Db 649 ATCATTTTACGTTTCCTCTCG-TCAGCTTTTATATCTAAGTGGCATTAATAAAGCAATT 590
QY 181 GCTTATCAATTTGTTGCAAGACAGTCACATATCAGTCAAAATAAATCATTTATTTGAT 240
Db 589 GCTTATCAATTTGTTGCAAGACAGTCACATATCAGTCAAAATAAATCATTTATTTGAT 530
QY 241 TTC 243
Db 529 TTC 527

RESULT 4
AQ990878/c
LOCUS
DEFINITION Rfc01715 Photorhabdus luminescens strain W14 M13 library
Photorhabdus luminescens genomic clone PLG01715, genomic survey sequence.
ACCESSION AQ990878
VERSION AQ990878.1 GI:9649472
KEYWORDS GSS.
SOURCE Photorhabdus luminescens
ORGANISM Photorhabdus luminescens
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales; Enterobacteriaceae; Photorhabdus.
REFERENCE 1 (bases 1 to 764)
AUTHORS ffrench-Constant, R.H., Waterfield, N., Burland, V., Perna, N.T., Daborn, P.J., Bowen, D. and Blattner, F.R.
TITLE A genomic sample sequence of the entomopathogenic bacterium Photorhabdus luminescens W14: potential implications for virulence
JOURNAL Appl. Environ. Microbiol. 66 (8), 3310-3329 (2000)
MEDLINE 20378633
PUBMED 10919786
COMMENT Contact: ffrench-Constant RH
Department of Biology and Biochemistry
University of Bath
South Building, Bath BA2 7AY, UK
Tel: (44) 1225 826621
Fax: (44) 1225 826779

Email: bsrfc@bath.ac.uk

This is one of 2,122 random reads from the M13 library. For annotation of identified clones (BLASTX, BLASTN and mapping to E. coli K12 genome) please see ffrench-Constant et al. 2000, Nucleic Acids Res.

Seq primer: M13 Forward

Class: shotgun.

FEATURES
source
1. .764
Location/Qualifiers
/organism="Photorhabdus luminescens"
/mol_type="genomic DNA"
/strain="W14"
/db_xref="taxon:29488"
/clone="PLG01715"
/dev_stage="primary phase variant"
/clone_lib="Photorhabdus luminescens strain W14 M13 library"
/note="Genomic DNA from strain W14 was size selected (1-2 kb) and then cloned into M13 Janus."

ORIGIN

Query Match 85.9%; Score 208.8; DB 28; Length 764;
Best Local Similarity 97.5%; Pred. No. 6.5e-30;
Matches 232; Conservative 0; Mismatches 4; Indels 2; Gaps 2;
QY 6 TACAGGTCACATAACCATCTAAGTAGTTCATTCATAGTGCATATGTTGTTT 65
Db 763 TACAGGTCACATAAACCATTAAAGTAGTTCATTCATAGTGCATATGTTGTTT 704
QY 66 CAGTATATGTTAGTCTCTGTTTTTATGCAAAATCTAAATTAATATATGATTTATATCA 125
Db 703 CAGTATATGTTAGTCTCTGTTTTTATGCAAAATCTAAATTAATATATGATTTATCA 645
QY 126 TTTTACGTTTCTCGTTCAGCTTTTATATCTAAGTGGCATTAATAAAGCAATTGCTTA 185
Db 644 TTTTACGTTTCTCGTTCAG-TTTTTATCTAAGTGGCATTAATAAAGCAATTGCTTA 586
QY 186 TCAATTTGTTGCAAGACAGTCACATATCAGTCAAAATAAATCATTTATTTGATTC 243
Db 585 TCAATTTGTTGCAAGACAGTCACATATCAGTCAAAATAAATCATTTATTTGATTC 528

RESULT 5
BQ157398/c
LOCUS
DEFINITION BQ157398 472 bp mRNA linear EST 24-APR-2002
NF104D07IR 5', mRNA sequence.
ACCESSION BQ157398
VERSION BQ157398.1 GI:20294457
KEYWORDS EST.
SOURCE Medicago truncatula (barrel medic)
ORGANISM Medicago truncatula
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae; Medicago.
REFERENCE 1 (bases 1 to 472)
AUTHORS Torres-Jerez, I., Scott, A.D., Harris, A.R., Gonzales, R.A., Bell, C.J., Flores, H.R., Inman, J.T., Weller, J.W. and May, G.D.
TITLE Expressed Sequence Tags from the Samuel Roberts Noble Foundation Medicago truncatula irradiated library
JOURNAL Unpublished (2001)
COMMENT Contact: May GD
Plant Biology Division
The Samuel Roberts Noble Foundation
2510 Sam Noble Parkway, Ardmore, OK 73402, USA
Tel: 580 221 7391
Fax: 580 221 7380
Email: gdmay@noble.org
Insert Length: 472 Std Error: 0.00
Plate: 104 row: D column: 07
Seq primer: TCACACAGGAACAGCTATGAC.
Location/Qualifiers

Tel:	(44) 1225 826621
Fax:	(44) 1225 826779
Email:	bssrfc@bath.ac.uk
This is one of 2,122 random reads from the M13 library. For annotation of identified clones (BLASTX, BLASTN and mapping to E.coli K12 genome) please see french-Constant et al. 2000, Nucleic Acids Res.	
Seq primer:	M13 Forward
Class:	shotgun.
FEATURES	Location/Qualifiers
source	1..751
	/organism="Photorhabdus luminescens"
	/mol_type="genomic DNA"
	/strain="W14"
	/db_xref="taxon:29488"
	/clone="PLG00126"
	/dev_stage="primary phase variant"
	/clone_lib="Photorhabdus luminescens strain W14 M13 library"
	/note="genomic DNA from strain W14 was size selected (1-2 kb) and then cloned into M13 Janus."
ORIGIN	
	Query Match 77.1%; Score 187.4; DB 28; Length 751;
	Best Local Similarity 95.5%; Pred.No. 6.7e-26;
	Matches 213; Conservative 0; Mismatches -8; Indels 2; Gaps 2
QY	21 CCATCTTAAGTAGTGTGATTCCATAGTCAGCTGCATATCTTGTTGGTTTACAGTATTATGTAGTC 80
Db	
QY	749 CCCATTAGAGTGTATTCATAG-CACTGCATATGTTGTTTTACAG-ATAATGTAGTC 692
Db	
QY	81 TGTTTTTTAAGCAAAATCTAATTTAATATATATGATATTTATATCATATTTACGTTTCGCT 140
Db	
QY	141 TCAGCTTTTTTATCTAAGTTGGCATTATAAAAGCATTCCTTATCAATTTGTTGCAAC 200
Db	
QY	631 TCAGCTTTTTTATANTAAGTTGGCATTATAAAAGCATTCCTTATCAATTTGTTGCAAC 572
Db	
QY	201 GAACAGTCACTATCAGTCAAATAAAATCATTTATTCGATTTC 243
Db	
QY	571 GAACAGTCACTATCAGTCAAATAAAATCATTTATTCGATTTC 529
Db	
RESULT 8	
AQ990346/c	
LOCUS	743 bp DNA linear GSS 14-AUG-2000
DEFINITION	Rfc01106 Photorhabdus luminescens strain W14 M13 library
	Photorhabdus luminescens genomic clone PLG01106, genomic survey sequence.
ACCESSION	AQ990346.1 GI:9648940
VERSION	AQ990346
KEYWORDS	GSS.
SOURCE	Photorhabdus luminescens
ORGANISM	Photorhabdus luminescens
	Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales; Enterobacteriaceae; Photorhabdus.
REFERENCE	1 (bases 1 to 743)
AUTHORS	french-Constant,R.H., Waterfield,N., Burland,V., Perna,N.T., Daborn,P.J., Bowen,D. and Blatner,F.R.
TITLE	A genomic sample sequence of the entomopathogenic bacterium Photorhabdus luminescens W14: potential implications for virulence
JOURNAL	Appl. Environ. Microbiol. 66 (8), 3310-3329 (2000)
MEDLINE	20378633
PUBMED	10919786
COMMENT	Contact: french-Constant RH Department of Biology and Biochemistry University of Bath South Building, Bath BA2 7AY, UK Tel: (44) 1225 826621 Fax: (44) 1225 826779 Email: bssrfc@bath.ac.uk This is one of 2,122 random reads from the M13 library. For

Yang, L., Yuan, Z., Zavolan, M., Zhu, Y., Zimmer, A., Carninci, P., Hayatsu, N., Hirozane-Kishikawa, T., Waki, K., Kawai, J., Nakamura, M., Sakazume, N., Sato, K., Shiraki, T., Waki, K., Kawai, J., Aizawa, K., Arakawa, T., Fukuda, S., Hara, A., Hashizume, M., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Miyazaki, A., Sakai, K., Sasaki, D., Shibata, K., Shinagawa, A., Yasunishi, A., Yoshino, M., Waterston, R., Lander, E.S., Rogers, J., Birney, E. and Hayashizaki, Y.

Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs

Nature 420, 563-573 (2002)

22354683

12466851

Contract: Yoshihide Hayashizaki

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Fax: 81-45-503-9216

Email: genome-res@gsc.riken.go.jp

URL: <http://genome.gsc.riken.go.jp/>

Aizawa, K., Akimura, T., Arakawa, T., Carninci, P., Fukuda, S., Hirozane, T., Imotani, K., Ishii, Y., Itoh, M., Kawai, J., Konno, H., Miyazaki, A., Murata, N., Nakamura, M., Nomura, K., Numazaki, R., Ohno, M., Sakai, K., Sakazume, N., Sasaki, D., Sato, K., Shibata, K., Shiraki, T., Tagami, M., Waki, K., Watahiki, A., Muramatsu, M. and Hayashizaki, Y. Direct Submission

Computational Analysis of Full-Length Mouse cDNAs Compared with Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)

Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000)

RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000)

Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)

cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.

Please visit our web site (<http://genome.gsc.riken.go.jp>) for further details.

FEATURES

source

1. .299

Location/Qualifiers

/organism="Mus musculus"

/mol_type="mRNA"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/clone="I430040C03"

/tissue_type="whole body"

/dev_stage="18 days embryo"

/clone_lib="RIKEN full-length enriched, 18 days embryo whole body"

ORIGIN

Query Match 76.4%; Score 185.6; DB 13; Length 299;

Best Local Similarity 97.9%; Pred. No. 28-25;

Matches 188; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 TCTGTTACAGGTCACCTAATACCATCTAAGTAGTTCATAGTCAGTCGATGTTGG 60

Db |||||

QY 108 TCTGTCACAGGTCACCTAATACCATCTAAGTAGTTCATAGTCAGTCGATGTTGG 167

Db |||||

QY 61 TTTTACAGTATTATGATGCTGTTTTTATGCAAAATCTAATTTATATATATTATTTA 120

Db |||||

QY 168 TTTTACAGTATTATGATGCTGTTTTTATGCAAAATCTAATTTATATATTATTTA 227

Db |||||

QY 121 TATCAATTTACGTTTCCTGTTACGCTTTTATATACATAGTGGCAATTAATAAAGCAAT 180

Db |||||

QY 228 TATCACTTTACGTTTCCTGTTACGCTTTTATATACATAGTGGCAATTAATAAAGCAAT 287

Db |||||

QY 181 GCTTATCAATTT 192

Db |||||

QY 288 GCTTATCAATTT 299

Db |||||

RESULT 10

AQ990861/c 753 bp DNA linear GSS 14-AUG-2000

LOCUS Rf001698 Photorhabdus luminescens strain W14 M13 library

DEFINITION Photorhabdus luminescens genomic clone FLG01698, genomic survey sequence.

ACCESSION AQ990861

VERSION AQ990861.1 GI:9649455

KEYWORDS GSS.

SOURCE Photorhabdus luminescens

ORGANISM Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales; Enterobacteriaceae; Photorhabdus.

REFERENCE 1 (bases 1 to 753)

AUTHORS fFrench-Constant, R.H., Waterfield, N., Burland, V., Perna, N.T., Daborn, P.J., Bowen, D. and Blattner, F.R.

TITLE A genomic sample sequence of the entomopathogenic bacterium Photorhabdus luminescens W14: potential implications for virulence

JOURNAL Appl. Environ. Microbiol. 66 (8), 3310-3329 (2000)

MEDLINE 20378633

PUBMED 10919786

COMMENT Contact: fFrench-Constant RH

Department of Biology and Biochemistry

University of Bath

South Building, Bath BA2 7AY, UK

Tel: (44) 1225 826621

Fax: (44) 1225 826779

Email: bssr@bath.ac.uk

This is one of 2,122 random reads from the M13 library. For annotation of identified clones (BLASTX, BLASTN and mapping to E. coli K12 genome) please see fFrench-Constant et al. 2000, Nucleic Acids Res

Seq primer: M13 Forward

Class: shotgun.

Location/Qualifiers

1. .753

/organism="Photorhabdus luminescens"

/mol_type="genomic DNA"

/strain="W14"

/db_xref="taxon:29488"

/clone="PLG01698"

/dev_stage="primary phase variant"

/clone_lib="Photorhabdus luminescens strain W14 M13 library"

/note="Genomic DNA from strain W14 was size selected (1-2 kb) and then cloned into M13 Janus."

ORIGIN

Query Match 72.1%; Score 175.2; DB 28; Length 753;

Best Local Similarity 95.5%; Pred. No. 1.3e-23;

Matches 210; Conservative 0; Mismatches 7; Indels 3; Gaps 3;

QY 24 TCTAAGTAGTTCATTCATAGTCAGTCGATATGTTGTTTTTACAGTATTATAGTCTGT 83

Db |||||

QY 751 TTTAAGTAGTTCATTCANAGTCACNG-ATATGTTGTTTACAG-ATAATGAGTCTGT 694

Db |||||

QY 84 TTTTATGCAAAATCTAATTTAATATATGATTTATATATATTTACGTTTCTGTTCA 143

Db |||||

QY 693 TTTTATGCAAAATCTAATTTAATATATGATTTATATATATTTACGTTTCTGTTCA 634

Db |||||

QY 144 GCTTTTTTATCTAAGTTGGCATTATAAAAAAGCAATGCTTATCAATTTGTTGCAACGAA 203

Db |||||

QY 633 GCTTTTTTATCTAAG-TGGCATTATAAAAAAGCAATGCTTATCAATTTGTTGCAACGAA 575

Db |||||

QY 204 CAGGTCATCATCAGTCAGTCAAAATATAAATCATTTATTTTC 243

Db |||||

QY 574 CAGGTCATCATCAGTCAGTCAAAATATAAATCATTTATTTTC 535

Db |||||

RESULT 11
 AQ990173/c
 LOCUS
 DEFINITION
 746 bp DNA linear GSS 14-AUG-2000
 RfC00898 Photorhabdus luminescens strain W14 M13 library
 Photorhabdus luminescens genomic clone PLG00898, genomic survey
 sequence.
 ACCESSION
 VERSION AQ990173.1 GI:9648767
 KEYWORDS
 SOURCE
 ORGANISM
 Photorhabdus luminescens
 Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 Enterobacteriaceae; Photorhabdus.
 REFERENCE
 1 (bases 1 to 746)
 AUTHORS
 ffrench-Constant, R.H., Waterfield, N., Burland, V., Perna, N.T.,
 Daborn, P.J., Bowen, D. and Blattner, F.R.
 TITLE
 A genomic sample sequence of the entomopathogenic bacterium
 Photorhabdus luminescens W14: potential implications for virulence
 JOURNAL
 MEDLINE
 PUBMED 20378633
 COMMENT
 Contact: ffrench-Constant RH
 10919786
 Department of Biology and Biochemistry
 University of Bath
 South Building, Bath BA2 7AY, UK
 Tel: (44) 1225 826621
 Fax: (44) 1225 826779
 Email: bssrfc@bath.ac.uk
 This is one of 2,122 random reads from the M13 library. For
 annotation of identified clones (BLASTX, BLASTN and mapping to E.
 coli K12 genome) please see ffrench-Constant et al. 2000, Nucleic
 Acids Res.
 Seq primer: M13 Forward
 Class: shotgun.
 FEATURES
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 1..746
 /organism="Photorhabdus luminescens"
 /mol_type="genomic DNA"
 /strain="W14"
 /db_xref="taxon:29488"
 /clone="PLG00898"
 /dev_stage="primary phase variant"
 /clone_lib="Photorhabdus luminescens strain W14 M13
 library"
 /notes="Genomic DNA from strain W14 was size selected (1-2
 kb) and then cloned into M13 Janus."
 ORIGIN
 Query Match 58.2%; Score 165.8; DB 28; Length 746;
 Best Local Similarity 97.4%; Pred. No. 7.5e-22;
 Matches 189; Conservative 0; Mismatches 3; Indels 2; Gaps 2;
 QY 51 ATATGTTGCTTTTACAGTATTATGAGTCGTGTTTTTATGCAAAATCTAATTAATATA 110
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 Db 723 ATATGTTGCTTTTACAG-ATTAATGAGTCGTGTTTTTATGCAAAATCTAATTAATATA 665
 |||||
 QY 111 TTGATATTTATATCATTTTACGTTTCGTCAGCTTTTTTATACATAAGTTGGCAATTATA 170
 |||||
 Db 664 TTGATATTTANATCATTTTACGTTTCGTTTCAGTTTTTTATATTAAGTTGGCAATTATA 605
 |||||
 QY 171 AAAAGCAATTGCTTATCAA-TTTGTTGCAAGCAAGTCAGTCATCATCAAGTCAAAATAAAT 229
 |||||
 Db 604 AAAAGCAATTGCTTATCAATTTTGTTCGAACGACAGTCAGTCATCATCAAGTCAAAATAAAT 545
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 QY 230 CATTAATTTGATTTTC 243
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 Db 544 CATTAATTTGATTTTC 531
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 RESULT 12
 AQ991774/c

LOCUS
 DEFINITION
 770 bp DNA linear GSS 14-AUG-2000
 RfC02039F Photorhabdus luminescens strain W14 M13 library
 Photorhabdus luminescens genomic clone PLG02039F, genomic survey
 sequence.
 ACCESSION
 VERSION AQ991774.1 GI:9650368
 KEYWORDS
 SOURCE
 ORGANISM
 Photorhabdus luminescens
 Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 Enterobacteriaceae; Photorhabdus.
 REFERENCE
 1 (bases 1 to 770)
 AUTHORS
 ffrench-Constant, R.H., Waterfield, N., Burland, V., Perna, N.T.,
 Daborn, P.J., Bowen, D. and Blattner, F.R.
 TITLE
 A genomic sample sequence of the entomopathogenic bacterium
 Photorhabdus luminescens W14: potential implications for virulence
 JOURNAL
 MEDLINE
 PUBMED 20378633
 COMMENT
 Contact: ffrench-Constant RH
 10919786
 Department of Biology and Biochemistry
 University of Bath
 South Building, Bath BA2 7AY, UK
 Tel: (44) 1225 826621
 Fax: (44) 1225 826779
 Email: bssrfc@bath.ac.uk
 This is one of a selected subset of flipped clones from the M13
 library. For annotation of identified clones (BLASTX, BLASTN and
 mapping to E. coli K12 genome) please see ffrench-Constant et al.
 2000, Nucleic Acids Res.
 Seq primer: M13 Reverse
 Class: shotgun.
 FEATURES
 source
 1..770
 /organism="Photorhabdus luminescens"
 /mol_type="genomic DNA"
 /strain="W14"
 /db_xref="taxon:29488"
 /clone="PLG02039F"
 /dev_stage="primary phase variant"
 /clone_lib="Photorhabdus luminescens strain W14 M13
 library"
 /notes="Genomic DNA from strain W14 was size selected (1-2
 kb) and then cloned into M13 Janus."
 ORIGIN
 Query Match 66.2%; Score 160.8; DB 28; Length 770;
 Best Local Similarity 98.8%; Pred. No. 6.4e-21;
 Matches 162; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 1 TCTGTTACAGGTCACATAATACCATCTAAGTAGTTGATTCATAGTACTGATATGTTGTG 60
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 Db 197 TCTGTTACAGGTCACATAATACCATCTAAGTAGTTGATTCATAGTACTGATATGTTGTG 138
 |||||
 QY 61 TTTTACAGTATTATGAGTCGTGTTTTTATGCAAAATCTAATTTAATATATGATATTTA 120
 |||||
 Db 137 TTTTACAGTATTATGAGTCGTGTTTTTATGCAAAATCTAATTTAATATATGATATTTA 78
 |||||
 QY 121 TATCATTTTACGTTTCTCGTTCAGCTTTTTTATACATAAGTTGGC 164
 |||||
 Db 77 TATCATTTTACGTTTCTCGTTCAGCTTTTTTATACATAACTTGAC 34
 |||||
 RESULT 13
 AQ991791/c
 LOCUS
 DEFINITION
 791 bp DNA linear GSS 14-AUG-2000
 RfC02368F Photorhabdus luminescens strain W14 M13 library
 Photorhabdus luminescens genomic clone PLG02368F, genomic survey
 sequence.
 ACCESSION
 VERSION AQ991791.1 GI:9650385
 KEYWORDS
 SOURCE
 ORGANISM
 Photorhabdus luminescens

ORGANISM Photorhabdus luminescens
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Photorhabdus.
REFERENCE 1 (bases 1 to 791)
AUTHORS ffrench-Constant,R.H., Waterfield,N., Burland,V., Perna,N.T.,
Daborn,P.J., Bowen,D. and Blattner,F.R.
TITLE A genomic sample sequence of the entomopathogenic bacterium
Photorhabdus luminescens W14: potential implications for virulence
JOURNAL Appl. Environ. Microbiol. 66 (8), 3310-3329 (2000)
MEDLINE 20378633
PUBMED 10919786
COMMENT Contact: ffrench-Constant RH
Department of Biology and Biochemistry
University of Bath
South Building, Bath BA2 7AY, UK
Tel: (44) 1225 826621
Fax: (44) 1225 826779
Email: bssrf@bath.ac.uk
This is one of a selected subset of flipped clones from the M13
library. For annotation of identified clones (BLASTX, BLASTN and
mapping to E. coli K12 genome) please see ffrench-Constant et al.
2000, Nucleic Acids Res.
Seq primer: M13 Reverse
Class: shotgun.
Location/Qualifiers
1..791
/organism="Photorhabdus luminescens"
/mol_type="genomic DNA"
/strain="W14"
/db_xref="taxon:29488"
/clone="PIG02368P"
/dev_stage="primary phase variant"
/clone_lib="Photorhabdus luminescens strain W14 M13
library"
/note="Genomic DNA from strain W14 was size selected (1-2
kb) and then cloned into M13 Janus."
FEATURES
source
Query Match 66.2%; Score 160.8; DB 28; Length 791;
Best Local Similarity 98.8%; Pred. No. 6.4e-21;
Matches 162; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
ORIGIN
1 TCTGTTACAGTCACTAATACATCTAAGTAGTTCGATTCATGACGACGATGCTGTCG 60
194 TCTGTTACAGTCACTAATACATCTAAGTAGTTCGATTCATGACGACGATGCTGTCG 135
61 TTTTACAGTATATGATGCTGTTTTTTATGCAAAATCTAATTTAATATATGATTTA 120
134 TTTTACAGTATATGATGCTGTTTTTTATGCAAAATCTAATTTAATATATGATTTA 75
121 TATCATTTTACGTTCTCGTTCAGCTTTTATATCTAAGTTGGC 164
74 TATCATTTTACGTTCTCGTTCAGCTTTTATATCTAAGTTGAC 31
RESULT 14
LOCUS AQ991039/c 695 bp DNA linear GSS 14-AUG-2000
DEFINITION Rf001894 Photorhabdus luminescens strain W14 M13 library
Photorhabdus luminescens genomic clone PIG01894, genomic survey
sequence.
ACCESSION AQ991039
VERSION AQ991039.1 GI:9649633
KEYWORDS GSS.
SOURCE Photorhabdus luminescens
ORGANISM Photorhabdus luminescens
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Photorhabdus.
REFERENCE 1 (bases 1 to 695)
AUTHORS ffrench-Constant,R.H., Waterfield,N., Burland,V., Perna,N.T.,
Daborn,P.J., Bowen,D. and Blattner,F.R.
TITLE A genomic sample sequence of the entomopathogenic bacterium
Photorhabdus luminescens W14: potential implications for virulence
JOURNAL Appl. Environ. Microbiol. 66 (8), 3310-3329 (2000)
MEDLINE 20378633
PUBMED 10919786
COMMENT Contact: ffrench-Constant RH
Department of Biology and Biochemistry
University of Bath
South Building, Bath BA2 7AY, UK
Tel: (44) 1225 826621
Fax: (44) 1225 826779
Email: bssrf@bath.ac.uk
This is one of a selected subset of flipped clones from the M13
library. For annotation of identified clones (BLASTX, BLASTN and
mapping to E. coli K12 genome) please see ffrench-Constant et al.
2000, Nucleic Acids Res.
Seq primer: M13 Reverse
Class: shotgun.
Location/Qualifiers
1..695
/organism="Photorhabdus luminescens"
/mol_type="genomic DNA"
/strain="W14"
/db_xref="taxon:29488"
/clone="PIG01894"
/dev_stage="primary phase variant"
/clone_lib="Photorhabdus luminescens strain W14 M13
library"
/note="Genomic DNA from strain W14 was size selected (1-2
kb) and then cloned into M13 Janus."
FEATURES
source
Query Match 65.6%; Score 159.4; DB 28; Length 695;
Best Local Similarity 99.4%; Pred. No. 1.2e-20;
Matches 160; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
ORIGIN
83 TTTTATGCAAAATCTAATTTAATATATGATTTATATATGATTTATGATTTACGTTTCGTTTC 142
695 TTTTATGCAAAATCTAATTTAATATATGATTTATATGATTTATGATTTACGTTTCGTTTC 636
143 AGCTTTTTTATGCTAAGTTGGCATTATATAAAGCAATGCTTATCAATTTGTTGCAACA 202
635 AGCTTTTTTATGCTAAGTTGGCATTATATAAAGCAATGCTTATCAATTTGTTGCAACA 576
203 ACAGTCACTATCAGTCAAAATATAATCATTTATTTGATTTTC 243
575 ACAGTCACTATCAGTCAAAATATAATCATTTATTTGATTTTC 535
RESULT 15
LOCUS AQ991352/c 719 bp DNA linear GSS 14-AUG-2000
DEFINITION Rf02270 Photorhabdus luminescens strain W14 M13 library
Photorhabdus luminescens genomic clone PIG02270, genomic survey
sequence.
ACCESSION AQ991352
VERSION AQ991352.1 GI:9649946
KEYWORDS GSS.
SOURCE Photorhabdus luminescens
ORGANISM Photorhabdus luminescens
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Photorhabdus.
REFERENCE 1 (bases 1 to 719)
AUTHORS ffrench-Constant,R.H., Waterfield,N., Burland,V., Perna,N.T.,
Daborn,P.J., Bowen,D. and Blattner,F.R.
TITLE A genomic sample sequence of the entomopathogenic bacterium
Photorhabdus luminescens W14: potential implications for virulence
JOURNAL Appl. Environ. Microbiol. 66 (8), 3310-3329 (2000)
MEDLINE 20378633
PUBMED 10919786
COMMENT Contact: ffrench-Constant RH
Department of Biology and Biochemistry
University of Bath
South Building, Bath BA2 7AY, UK
Tel: (44) 1225 826621

JOURNAL Appl. Environ. Microbiol. 66 (8), 3310-3329 (2000)
MEDLINE 20378633
PUBMED 10919786
COMMENT Contact: ffrench-Constant RH
Department of Biology and Biochemistry
University of Bath
South Building, Bath BA2 7AY, UK
Tel: (44) 1225 826621
Fax: (44) 1225 826779
Email: bssrf@bath.ac.uk
This is one of 2,122 random reads from the M13 library. For
annotation of identified clones (BLASTX, BLASTN and mapping to E.
coli K12 genome) please see ffrench-Constant et al. 2000, Nucleic
Acids Res.
Seq primer: M13 Forward
Class: shotgun.
Location/Qualifiers
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/organism="Photorhabdus luminescens"
/mol_type="genomic DNA"
/strain="W14"
/db_xref="taxon:29488"
/clone="PIG01894"
/dev_stage="primary phase variant"
/clone_lib="Photorhabdus luminescens strain W14 M13
library"
/note="Genomic DNA from strain W14 was size selected (1-2
kb) and then cloned into M13 Janus."
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Best Local Similarity 99.4%; Pred. No. 1.2e-20;
Matches 160; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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83 TTTTATGCAAAATCTAATTTAATATATGATTTATATGATTTATGATTTACGTTTCGTTTC 142
695 TTTTATGCAAAATCTAATTTAATATATGATTTATATGATTTATGATTTACGTTTCGTTTC 636
143 AGCTTTTTTATGCTAAGTTGGCATTATATAAAGCAATGCTTATCAATTTGTTGCAACA 202
635 AGCTTTTTTATGCTAAGTTGGCATTATATAAAGCAATGCTTATCAATTTGTTGCAACA 576
203 ACAGTCACTATCAGTCAAAATATAATCATTTATTTGATTTTC 243
575 ACAGTCACTATCAGTCAAAATATAATCATTTATTTGATTTTC 535
RESULT 15
LOCUS AQ991352/c 719 bp DNA linear GSS 14-AUG-2000
DEFINITION Rf02270 Photorhabdus luminescens strain W14 M13 library
Photorhabdus luminescens genomic clone PIG02270, genomic survey
sequence.
ACCESSION AQ991352
VERSION AQ991352.1 GI:9649946
KEYWORDS GSS.
SOURCE Photorhabdus luminescens
ORGANISM Photorhabdus luminescens
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Photorhabdus.
REFERENCE 1 (bases 1 to 719)
AUTHORS ffrench-Constant,R.H., Waterfield,N., Burland,V., Perna,N.T.,
Daborn,P.J., Bowen,D. and Blattner,F.R.
TITLE A genomic sample sequence of the entomopathogenic bacterium
Photorhabdus luminescens W14: potential implications for virulence
JOURNAL Appl. Environ. Microbiol. 66 (8), 3310-3329 (2000)
MEDLINE 20378633
PUBMED 10919786
COMMENT Contact: ffrench-Constant RH
Department of Biology and Biochemistry
University of Bath
South Building, Bath BA2 7AY, UK
Tel: (44) 1225 826621

Fax: (44) 1225 826779
Email: bsrfc@bath.ac.uk
This is one of 2,122 random reads from the M13 library. For
annotation of identified clones (BLASTX, BLASTN and mapping to E.
coli K12 genome) please see french-Constant et al. 2000, Nucleic
Acids Res.
Seq primer: M13 Forward
Class: shotgun.
Location/Qualifiers
1..719
/organism="Photorhabdus luminescens"
/mol_type="genomic DNA"
/strain="W14"
/db_xref="taxon:29488"
/clone="PLG02270"
/dev_stage="primary phase variant"
/clone_lib="Photorhabdus luminescens strain W14 M13
library"
/note="Genomic DNA from strain W14 was size selected (1-2
kb) and then cloned into M13 Janus."

ORIGIN

Query Match 65.4%; Score 159; DB 28; Length 719;
Best Local Similarity 97.3%; Pred. No. 1.4e-20;
Matches 181; Conservative 0; Mismatches 3; Indels 2; Gaps 2;
QY 58 GTGTTTACAGTATATAGTCTGTTTTCATGCAAAATCTAATTTAAATATATGATAT 117
Db 718 GTGTTTACAGTATATAGTCTGTTTTCATGCAAAATCTAATTTAAATATATGATAT 660
QY 118 TTATATCAATTTAGCTTCTCGTTTCAGCTTTTATATCTAAGTTGGCATTATAAAAAAGC 177
Db 659 TTATATCAATTTAGCTTCTCGTTTCAGCTTTTATATCTAAGTTGGCATTATAAAAAAGC 601
QY 178 ATTGCTTATCAATTTGTGCAACGAAAGGTCACATATCAGTCAAAATAAAATCATTATTT 237
Db 600 ATTGCTTATCAATTTGTGCAACGAAAGGTCACATATCAGTCAAAATAAAATCATTATTT 541
QY 238 GATTTC 243
Db 540 GATTTC 535

Search completed: September 9, 2004, 21:18:23
Job time : 1964.91 secs

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: September 9, 2004, 19:34:38 ; Search time 306.981 Seconds
(without alignments)
3982.858 Million cell updates/sec

Title: US-10-082-772B-2

Perfect score: 243

Sequence: 1 tcgttacaggtcactaata.....taaaatcattattgatttc 243

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 3304383 seqs, 2515761380 residues

Total number of hits satisfying chosen parameters: 6608766

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database : Published Applications NA:*

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4: /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq.*
5: /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq.*
6: /cgn2_6/ptodata/2/pubpna/PCTUS_PUBCOMB.seq.*
7: /cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq.*
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12: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq.*
13: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq2.*
14: /cgn2_6/ptodata/2/pubpna/US10A_PUBCOMB.seq.*
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16: /cgn2_6/ptodata/2/pubpna/US10C_PUBCOMB.seq.*
17: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq.*
18: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq.*
19: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	243	100.0	243	13	US-10-403-232-173
2	243	100.0	243	17	US-10-310-695-14
3	243	100.0	248	17	US-10-627-711-8
4	243	100.0	282	15	US-10-161-403-72
C 5	243	100.0	1763	11	US-09-244-805-57
C 6	243	100.0	1763	11	US-09-245-277-57
C 7	243	100.0	1763	17	US-10-792-481-57
8	243	100.0	4346	15	US-10-161-403-113
9	238.2	98.0	243	17	US-10-310-695-2
10	231	95.1	2959	13	US-10-270-176-8
11	231	95.1	3663	13	US-10-270-176-3
12	231	95.1	3695	13	US-10-270-176-13
13	231	95.1	4782	13	US-10-270-176-20
14	231	95.1	5646	13	US-10-270-176-41

15	231	95.1	5706	13	US-10-270-176-40	Sequence 40, Appl
16	231	95.1	5739	13	US-10-270-176-9	Sequence 9, Appl
17	231	95.1	5771	13	US-10-270-176-34	Sequence 34, Appl
18	231	95.1	5771	13	US-10-270-176-35	Sequence 35, Appl
19	231	95.1	5814	13	US-10-270-176-37	Sequence 37, Appl
20	231	95.1	5911	13	US-10-270-176-42	Sequence 42, Appl
21	231	95.1	5929	13	US-10-270-176-45	Sequence 45, Appl
22	231	95.1	5929	13	US-10-270-176-46	Sequence 46, Appl
23	231	95.1	5948	13	US-10-270-176-21	Sequence 21, Appl
24	231	95.1	5986	13	US-10-270-176-36	Sequence 21, Appl
25	231	95.1	6200	13	US-10-270-176-38	Sequence 36, Appl
26	231	95.1	6664	13	US-10-270-176-1	Sequence 38, Appl
27	231	95.1	6668	13	US-10-270-176-1	Sequence 1, Appl
28	231	95.1	6742	13	US-10-270-176-2	Sequence 2, Appl
C 29	226.8	93.3	4470	15	US-10-270-176-19	Sequence 19, Appl
C 30	226.8	93.3	4892	16	US-10-151-690-21	Sequence 21, Appl
31	226.8	93.3	5584	15	US-10-357-268-1	Sequence 1, Appl
32	226.8	93.3	17862	15	US-10-151-690-61	Sequence 61, Appl
C 33	226.8	93.3	17862	15	US-10-055-001A-23	Sequence 23, Appl
34	226.8	93.3	18691	15	US-10-055-001A-23	Sequence 23, Appl
C 35	226.8	93.3	18691	15	US-10-055-001A-13	Sequence 13, Appl
36	226.6	93.3	233	13	US-10-301-849A-16	Sequence 13, Appl
C 37	226.6	93.3	233	13	US-10-403-232-177	Sequence 16, Appl
38	225.4	92.8	4428	15	US-10-151-690-62	Sequence 177, App
39	225.4	92.8	4470	15	US-10-151-690-21	Sequence 62, Appl
40	225.4	92.8	4627	15	US-10-151-690-63	Sequence 21, Appl
41	225.4	92.8	4627	15	US-10-151-690-64	Sequence 63, Appl
42	225.4	92.8	4892	16	US-10-357-268-1	Sequence 64, Appl
C 43	225.4	92.8	5584	15	US-10-151-690-61	Sequence 1, Appl
44	225	92.6	233	13	US-10-151-690-61	Sequence 61, Appl
C 45	220.4	90.7	4428	15	US-10-403-232-179	Sequence 179, App
					US-10-151-690-62	Sequence 62, Appl

ALIGNMENTS

RESULT 1
US-10-403-232-173
; Sequence 173, Application US/10403232
; Publication No. US20030226164A1
; GENERAL INFORMATION:
; APPLICANT: Suttie, Janet Louise
; APPLICANT: Chilton, Mary-Dell
; APPLICANT: Que, Quideng
; APPLICANT: de Framond, Anic
; TITLE OF INVENTION: Lambda Integrase Mediated Recombination In Plants
; FILE REFERENCE: 70005USPS
; CURRENT APPLICATION NUMBER: US/10/403,232
; CURRENT FILING DATE: 2003-03-28
; NUMBER OF SEQ ID NOS: 185
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 173
; LENGTH: 243
; TYPE: DNA
; ORGANISM: Bacteriophage lambda
US-10-403-232-173

Query Match	100.0%;	Score 243;	DB 13;	Length 243;
Best Local Similarity	100.0%;	Pred. No. 1e-40;		
Matches 243;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
Qy	1	TCGTTCACAGTCACTAATACCATCTAAGTAGTGTGATTCATAGTACTGATGATTTGTG	60	
Db	1	TCGTTCACAGTCACTAATACCATCTAAGTAGTGTGATTCATAGTACTGATGATTTGTG	60	
Qy	61	TTTTCACAGTATTAGTACTCTGTTTTTATGCAAAATCTAATTATATATTGATTTTA	120	
Db	61	TTTTCACAGTATTAGTACTCTGTTTTTATGCAAAATCTAATTATATATTGATTTTA	120	
Qy	121	TATCATTTTACGTTCTCTCGTTTCAGCTTTTTTATACAAAGTTGGCATTATAAAAGCATT	180	
Db	121	TATCATTTTACGTTCTCTCGTTTCAGCTTTTTTATACAAAGTTGGCATTATAAAAGCATT	180	

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QY 181 GCTTATCAATTTGTTGCAACGACAGGTCACATCATCAGTCAGTCAAAATATAAATCATTATTGAT 240
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Db 181 GCTTATCAATTTGTTGCAACGACAGGTCACATCATCAGTCAGTCAAAATATAAATCATTATTGAT 240
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QY 241 TTC 243
    |||
Db 241 TTC 243

RESULT 2
US-10-310-695-14
; Sequence 14, Application US/10310695
; Publication No. US20040110293A1
; GENERAL INFORMATION:
; APPLICANT: DROGE, PETER
; APPLICANT: ENENKEL, BARBARA
; TITLE OF INVENTION: SEQUENCE SPECIFIC DNA RECOMBINATION IN EUKARYOTIC CELLS
; FILE REFERENCE: DEB:019JS
; CURRENT APPLICATION NUMBER: US/10/310,695
; CURRENT FILING DATE: 2002-12-05
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 14
; LENGTH: 243
; TYPE: DNA
; ORGANISM: Bacteriophage lambda
US-10-310-695-14

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Query Match 100.0%; Score 243; DB 17; Length 243;
Best Local Similarity 100.0%; Pred. No. 1e-40;
Matches 243; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCTGTTACAGGTCACATCAATCAATCAATCAATCAATCAATCAATCAATCAATCAATCAATCAAT 60
Db 1 TCTGTTACAGGTCACATCAATCAATCAATCAATCAATCAATCAATCAATCAATCAATCAATCAAT 60
QY 61 TTTTACAGTATTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 120
Db 61 TTTTACAGTATTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 120
QY 121 TATCATTATCAATTTCTCGTTTCAGTCTGTTTATGCAAAATCTAAATTAATATATGATATTTA 180
Db 121 TATCATTATCAATTTCTCGTTTCAGTCTGTTTATGCAAAATCTAAATTAATATATGATATTTA 180
QY 181 GCTTATCAATTTGTTGCAACGACAGGTCACATCATCAGTCAGTCAAAATATAAATCATTATTGAT 240
Db 181 GCTTATCAATTTGTTGCAACGACAGGTCACATCATCAGTCAGTCAAAATATAAATCATTATTGAT 240
QY 241 TTC 243
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Db 241 TTC 243

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RESULT 3
US-10-627-711-8
; Sequence 8, Application US/10627711
; Publication No. US20040115812A1
; GENERAL INFORMATION:
; APPLICANT: YANG, Shuwei
; TITLE OF INVENTION: METHODS AND NUCLEIC ACID VECTORS FOR RAPID EXPRESSION AND SCREENING OF CDNA CLONES
; FILE REFERENCE: 51236US
; CURRENT APPLICATION NUMBER: US/10/627,711
; CURRENT FILING DATE: 2003-07-28
; PRIOR APPLICATION NUMBER: 60/398,589
; PRIOR FILING DATE: 2002-07-26
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 8
; LENGTH: 248
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:

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; OTHER INFORMATION: primer
US-10-627-711-8

Query Match 100.0%; Score 243; DB 17; Length 248;
Best Local Similarity 100.0%; Pred. No. 1e-40;
Matches 243; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCTGTTACAGGTCACATCAATCAATCAATCAATCAATCAATCAATCAATCAATCAATCAATCAAT 60
Db 1 TCTGTTACAGGTCACATCAATCAATCAATCAATCAATCAATCAATCAATCAATCAATCAATCAAT 65
QY 61 TTTTACAGTATTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 120
Db 61 TTTTACAGTATTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 125
QY 121 TATCATTATCAATTTCTCGTTTCAGTCTGTTTATGCAAAATCTAAATTAATATATGATATTTA 150
Db 121 TATCATTATCAATTTCTCGTTTCAGTCTGTTTATGCAAAATCTAAATTAATATATGATATTTA 185
QY 181 GCTTATCAATTTGTTGCAACGACAGGTCACATCATCAGTCAGTCAAAATATAAATCATTATTGAT 240
Db 181 GCTTATCAATTTGTTGCAACGACAGGTCACATCATCAGTCAGTCAAAATATAAATCATTATTGAT 245
QY 241 TTC 243
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Db 241 TTC 248

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RESULT 4
US-10-161-403-72
; Sequence 72, Application US/10161403
; Publication No. US20030119104A1
; GENERAL INFORMATION:
; APPLICANT: Perkins, Edward
; APPLICANT: Perez, Carl
; APPLICANT: Lindenbaum, Michael
; APPLICANT: Greene, Amy
; APPLICANT: Leung, Josephine
; APPLICANT: Fleming, Elena
; APPLICANT: Stewart, Sandra
; APPLICANT: Shellard, Joan
; TITLE OF INVENTION: CHROMOSOME-BASED PLATFORMS
; FILE REFERENCE: 24601-420
; CURRENT APPLICATION NUMBER: US/10/161,403
; CURRENT FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: 60/294,758
; PRIOR FILING DATE: 2001-05-30
; PRIOR APPLICATION NUMBER: 60/366,891
; PRIOR FILING DATE: 2002-03-21
; NUMBER OF SEQ ID NOS: 129
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 72
; LENGTH: 282
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: attp
US-10-161-403-72

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Query Match 100.0%; Score 243; DB 15; Length 282;
Best Local Similarity 100.0%; Pred. No. 1.1e-40;
Matches 243; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCTGTTACAGGTCACATCAATCAATCAATCAATCAATCAATCAATCAATCAATCAATCAATCAAT 60
Db 15 TCTGTTACAGGTCACATCAATCAATCAATCAATCAATCAATCAATCAATCAATCAATCAATCAAT 74
QY 61 TTTTACAGTATTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 120
Db 75 TTTTACAGTATTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 134
QY 121 TATCATTATCAATTTCTCGTTTCAGTCTGTTTATGCAAAATCTAAATTAATATATGATATTTA 180
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Db 135 TATCATTTTACGTTTCTCGTTCAGCTTTTATATACTAAGTTGGCATTATAAAAAAGCATT 194
QY 181 GCTTATCAATTTGTTGCAAGAACAGTCTACATATCAGTCAAAATAAATCAATATTATTTGAT 240
Db 195 GCTTATCAATTTGTTGCAAGAACAGTCTACATATCAGTCAAAATAAATCAATATTATTTGAT 254
QY 241 TTC 243
Db 255 TTC 257

RESULT 5

US-09-244-805-57/c

; Sequence 57, Application US/09244805

; Publication No. US20030203840A1

; GENERAL INFORMATION:

; APPLICANT: Worley, Paul F.

; APPLICANT: Lanahan, Anthony

; APPLICANT: Goetz, Bernard

; APPLICANT: Heimisch, Holger

; APPLICANT: Kuner, Rohini

; APPLICANT: Scheek, Sigrid

; APPLICANT: Nikolic, Karoly

; APPLICANT: Zhukovski, Eugene

; TITLE OF INVENTION: IMMEDIATE EARLY GENES AND METHODS OF USE

; FILE REFERENCE: THEREFOR

; FILE REFERENCE: 10496/004001

; CURRENT APPLICATION NUMBER: US/09/244,805

; EARLIER FILING DATE: 1999-02-05

; EARLIER FILING DATE: 1998-02-12

; EARLIER FILING DATE: 1998-02-12

; EARLIER FILING DATE: 1998-02-06

; NUMBER OF SEQ ID NOS: 62

; SOFTWARE: FastSEQ for Windows Version 4.0

; SEQ ID NO 57

; LENGTH: 1763

; TYPE: DNA

; ORGANISM: Eukaryote

; FEATURE:

; NAME/KEY: misc_feature

; LOCATION: (1)...(1763)

; OTHER INFORMATION: Y = C or T

; OTHER INFORMATION: n = A,T,C or G

US-09-244-805-57

Query Match 100.0%; Score 243; DB 11; Length 1763;
Best Local Similarity 100.0%; Pred. No. 1.9e-40;
Matches 243; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCTGTTACAGTCACTAATACCACTAAGTAGTGTGATTCATAGTCACTGCTGATATGTTGTG 60
Db 431 TCTGTTACAGTCACTAATACCACTAAGTAGTGTGATTCATAGTCACTGCTGATATGTTGTG 372
QY 61 TTTTACAGTATATGATGTCTGTTTTTATGCAAAATCTAATTTAATATATTTGATATTTA 120
Db 371 TTTTACAGTATATGATGTCTGTTTTTATGCAAAATCTAATTTAATATATTTGATATTTA 312
QY 121 TATCATTTTACGTTTCTCGTTACGTTTATATCTAAGTTGGCATTATAAAAAAGCATT 180
Db 311 TATCATTTTACGTTTCTCGTTACGTTTATATCTAAGTTGGCATTATAAAAAAGCATT 252
QY 181 GCTTATCAATTTGTTGCAAGAACAGTCTATCAGTCAAAATAAATCAATATTATTTGAT 240
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QY 241 TTC 243
Db 191 TTC 189

RESULT 6

US-09-245-277-57/c

; Sequence 57, Application US/09245277
; Publication No. US20030211984A1
; GENERAL INFORMATION:
; APPLICANT: Worley, Paul F.
; APPLICANT: Lanahan, Anthony
; TITLE OF INVENTION: IMMEDIATE EARLY GENES AND METHODS OF USE
; FILE REFERENCE: THEREFOR
; FILE REFERENCE: JHU1530-3
; CURRENT APPLICATION NUMBER: US/09/245,277
; CURRENT FILING DATE: 1999-02-05
; PRIOR APPLICATION NUMBER: 60/074,518
; PRIOR FILING DATE: 1998-02-12
; PRIOR APPLICATION NUMBER: 60/074,135
; PRIOR FILING DATE: 1998-02-06
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 57
; LENGTH: 1763
; TYPE: DNA
; ORGANISM: Eukaryote
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(1763)
; OTHER INFORMATION: Y = C or T
; OTHER INFORMATION: n = A,T,C or G

US-09-245-277-57

Query Match 100.0%; Score 243; DB 11; Length 1763;
Best Local Similarity 100.0%; Pred. No. 1.9e-40;
Matches 243; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCTGTTACAGTCACTAATACCACTAAGTAGTGTGATTCATAGTCACTGCTGATATGTTGTG 60
Db 431 TCTGTTACAGTCACTAATACCACTAAGTAGTGTGATTCATAGTCACTGCTGATATGTTGTG 372
QY 61 TTTTACAGTATATGATGTCTGTTTTTATGCAAAATCTAATTTAATATATTTGATATTTA 120
Db 371 TTTTACAGTATATGATGTCTGTTTTTATGCAAAATCTAATTTAATATATTTGATATTTA 312
QY 121 TATCATTTTACGTTTCTCGTTACGTTTATATCTAAGTTGGCATTATAAAAAAGCATT 180
Db 311 TATCATTTTACGTTTCTCGTTACGTTTATATCTAAGTTGGCATTATAAAAAAGCATT 252
QY 181 GCTTATCAATTTGTTGCAAGAACAGTCACTATCAGTCAAAATAAATCAATATTATTTGAT 240
Db 251 GCTTATCAATTTGTTGCAAGAACAGTCACTATCAGTCAAAATAAATCAATATTATTTGAT 192
QY 241 TTC 243
Db 191 TTC 189

RESULT 7

US-10-792-481-57/c

; Sequence 57, Application US/10792481

; Publication No. US20040152658A1

; GENERAL INFORMATION:

; APPLICANT: Worley, Paul F.

; APPLICANT: Lanahan, Anthony

; APPLICANT: Goetz, Bernard

; APPLICANT: Heimisch, Holger

; APPLICANT: Kuner, Rohini

; APPLICANT: Scheek, Sigrid

; APPLICANT: Nikolic, Karoly

; APPLICANT: Zhukovski, Eugene

; TITLE OF INVENTION: IMMEDIATE EARLY GENES AND METHODS OF USE

; FILE REFERENCE: THEREFOR

; FILE REFERENCE: 10496/004001

; CURRENT APPLICATION NUMBER: US/10/792,481

; CURRENT FILING DATE: 2004-03-02

; PRIOR APPLICATION NUMBER: US/09/244,805

; PRIOR FILING DATE: 1999-02-05

; PRIOR APPLICATION NUMBER: 60/074,518

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; PRIOR FILING DATE: 1998-02-12
; PRIOR APPLICATION NUMBER: 60/074,135
; PRIOR FILING DATE: 1998-02-06
; NUMBER OF SEQ ID NOS: 62
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 57
; LENGTH: 1763
; TYPE: DNA
; ORGANISM: Eukaryote
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)...(1763)
; OTHER INFORMATION: Y = C or T
; OTHER INFORMATION: n = A,T,C or G
US-10-792-481-57

Query Match
Best Local Similarity 100.0%; Score 243; DB 17; Length 1763;
Matches 243; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCTGTTACAGGTCACCTAATACCATCTAAGTAGTGTGATTCATAGTGCATCATATGTTGTG 60
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QY 61 TTTTACAGTATTATGATCTGTTTTTATGCAAAATCTAAATTTAATATATGATATTTA 120
Db 371 TTTTACAGTATTATGATCTGTTTTTATGCAAAATCTAAATTTAATATATGATATTTA 312

QY 121 TATCATTTTACGTTTCTCGTTCAGCTTTTATACATAAGTTGGCATTATAAAAAAGCATT 180
Db 311 TATCATTTTACGTTTCTCGTTCAGCTTTTATACATAAGTTGGCATTATAAAAAAGCATT 252

QY 181 GCTTATCAATTTGTTGCAAGACAGTCACATCATAGTCAAAATATAAAATCATTTTGGAT 240
Db 251 GCTTATCAATTTGTTGCAAGACAGTCACATCATAGTCAAAATATAAAATCATTTTGGAT 192

QY 241 TTC 243
Db 191 TTC 189

RESULT 8
US-10-161-403-113
; Sequence 113, Application US/10161403
; Publication No. US20030119104A1
; GENERAL INFORMATION:
; APPLICANT: Perkins, Edward
; APPLICANT: Perez, Carl
; APPLICANT: Lindenbaum, Michael
; APPLICANT: Greene, Amy
; APPLICANT: Leung, Josephine
; APPLICANT: Fleming, Elena
; APPLICANT: Stewart, Sandra
; APPLICANT: Shellard, Joan
; TITLE OF INVENTION: CHROMOSOME-BASED PLATFORMS
; FILE REFERENCE: 24601-420
; CURRENT APPLICATION NUMBER: US/10/161,403
; CURRENT FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: 60/294,758
; PRIOR FILING DATE: 2001-05-30
; PRIOR APPLICATION NUMBER: 60/366,891
; PRIOR FILING DATE: 2002-03-21
; NUMBER OF SEQ ID NOS: 129
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 113
; LENGTH: 4346
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: pSV40-193AttppsensePur Plasmid
US-10-161-403-113

Query Match
100.0%; Score 243; DB 15; Length 4346;
US-10-161-403-113
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Best Local Similarity 100.0%; Pred. No. 2.6e-40;
Matches 243; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCTGTTACAGGTCACCTAATACCATCTAAGTAGTGTGATTCATAGTGCATCATATGTTGTG 60
Db 4070 TCTGTTACAGGTCACCTAATACCATCTAAGTAGTGTGATTCATAGTGCATCATATGTTGTG 4129

QY 61 TTTTACAGTATTATGATCTGTTTTTATGCAAAATCTAAATTTAATATATGATATTTA 120
Db 4130 TTTTACAGTATTATGATCTGTTTTTATGCAAAATCTAAATTTAATATATGATATTTA 4189

QY 121 TATCATTTTACGTTTCTCGTTCAGCTTTTATACATAAGTTGGCATTATAAAAAAGCATT 180
Db 4190 TATCATTTTACGTTTCTCGTTCAGCTTTTATACATAAGTTGGCATTATAAAAAAGCATT 4249

QY 181 GCTTATCAATTTGTTGCAAGACAGTCACATCATAGTCAAAATATAAAATCATTTTGGAT 240
Db 4250 GCTTATCAATTTGTTGCAAGACAGTCACATCATAGTCAAAATATAAAATCATTTTGGAT 4309

QY 241 TTC 243
Db 4310 TTC 4312

RESULT 9
US-10-310-695-2
; Sequence 2, Application US/10310695
; Publication No. US20040110293A1
; GENERAL INFORMATION:
; APPLICANT: ENENKEL, BARBARA
; APPLICANT: DROGE, PETER
; TITLE OF INVENTION: SEQUENCE SPECIFIC DNA RECOMBINATION IN EUKARYOTIC CELLS
; FILE REFERENCE: DEBR-019US
; CURRENT APPLICATION NUMBER: US/10/310,695
; CURRENT FILING DATE: 2002-12-05
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 243
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Primer
US-10-310-695-2

Query Match
98.0%; Score 238.2; DB 17; Length 243;
Best Local Similarity 98.8%; Pred. No. 1e-39;
Matches 240; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 TCTGTTACAGGTCACCTAATACCATCTAAGTAGTGTGATTCATAGTGCATCATATGTTGTG 60
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QY 61 TTTTACAGTATTATGATCTGTTTTTATGCAAAATCTAAATTTAATATATGATATTTA 120
Db 61 TTTTACAGTATTATGATCTGTTTTTATGCAAAATCTAAATTTAATATATGATATTTA 120

QY 121 TATCATTTTACGTTTCTCGTTCAGCTTTTATACATAAGTTGGCATTATAAAAAAGCATT 180
Db 121 TATCATTTTACGTTTCTCGTTCAGCTTTTATACATAAGTTGGCATTATAAAAAAGCATT 180

QY 181 GCTTATCAATTTGTTGCAAGACAGTCACATCATAGTCAAAATATAAAATCATTTTGGAT 240
Db 181 GCTTATCAATTTGTTGCAAGACAGTCACATCATAGTCAAAATATAAAATCATTTTGGAT 240

QY 241 TTC 243
Db 241 TTC 243

RESULT 10
US-10-270-176-8
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; Sequence 8, Application US/10270176
; Publication No. US20040033608A1
; GENERAL INFORMATION:
; APPLICANT: Wanner, Barry
; APPLICANT: Haldemann, Andreas
; TITLE OF INVENTION: PLASMIDS, STRAINS, AND METHODS OF USE
; FILE REFERENCE: 290.00140101
; CURRENT APPLICATION NUMBER: US/10/270,176
; PRIOR FILING DATE: 2002-10-10
; PRIOR APPLICATION NUMBER: 60/328,642
; PRIOR FILING DATE: 2001-10-10
; PRIOR APPLICATION NUMBER: 60/375,059
; PRIOR FILING DATE: 2002-04-24
; NUMBER OF SEQ ID NOS: 118
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 8
; LENGTH: 2959
; TYPE: DNA
; ORGANISM: artificial
; FEATURE:
; OTHER INFORMATION: CRIM plasmid
US-10-270-176-8

Query Match      95.1%; Score 231; DB 13; Length 2959;
Best Local Similarity 99.2%; Pred. No. 6.6e-38;
Matches 243; Conservative 0; Mismatches 0; Indels 2; Gaps 1;

QY 1 TCTGTTACAGGTCACCTAATACCATCTTAAGTAGTTCATAGTACGACTGC--ATATGTTG 58
Db 939 TCTGTTACAGGTCACCTAATACCATCTTAAGTAGTTCATAGTACGACTGCATATATGTTG 998

QY 59 TGTGTTACAGTATTATGTAAGTCTGTTTTTATGCAAAATCTAATTTAATATATGATATT 118
Db 999 TGTGTTACAGTATTATGTAAGTCTGTTTTTATGCAAAATCTAATTTAATATATGATATT 1058

QY 119 TATATCATTTTACGTTTCTCGTTCAGCTTTTATATACTAAGTTGGCAATATAAAAAAGCA 178
Db 1059 TATATCATTTTACGTTTCTCGTTCAGCTTTTATATACTAAGTTGGCAATATAAAAAAGCA 1118

QY 179 TTGCTTATCAATTTGTTGCAACGACGTCACCTATCAGTCAAAATCAATTTAATATGATATT 238
Db 1119 TTGCTTATCAATTTGTTGCAACGACGTCACCTATCAGTCAAAATCAATTTAATATGATATT 1178

QY 239 ATTTC 243
Db 1179 ATTTC 1183

RESULT 11
US-10-270-176-3
; Sequence 3, Application US/10270176
; Publication No. US20040033608A1
; GENERAL INFORMATION:
; APPLICANT: Wanner, Barry
; APPLICANT: Haldemann, Andreas
; TITLE OF INVENTION: PLASMIDS, STRAINS, AND METHODS OF USE
; FILE REFERENCE: 290.00140101
; CURRENT APPLICATION NUMBER: US/10/270,176
; CURRENT FILING DATE: 2002-10-10
; PRIOR APPLICATION NUMBER: 60/328,642
; PRIOR FILING DATE: 2001-10-10
; PRIOR APPLICATION NUMBER: 60/375,059
; PRIOR FILING DATE: 2002-04-24
; NUMBER OF SEQ ID NOS: 118
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 3
; LENGTH: 3663
; TYPE: DNA
; ORGANISM: artificial
; FEATURE:
; OTHER INFORMATION: CRIM plasmid
US-10-270-176-3

Query Match      95.1%; Score 231; DB 13; Length 3663;
Best Local Similarity 99.2%; Pred. No. 7.1e-38;
Matches 243; Conservative 0; Mismatches 0; Indels 2; Gaps 1;

QY 1 TCTGTTACAGGTCACCTAATACCATCTTAAGTAGTTCATAGTACGACTGC--ATATGTTG 58
Db 1643 TCTGTTACAGGTCACCTAATACCATCTTAAGTAGTTCATAGTACGACTGCATATATGTTG 1702

QY 59 TGTGTTACAGTATTATGTAAGTCTGTTTTTATGCAAAATCTAATTTAATATATGATATT 118
Db 1703 TGTGTTACAGTATTATGTAAGTCTGTTTTTATGCAAAATCTAATTTAATATATGATATT 1762

QY 119 TATATCATTTTACGTTTCTCGTTCAGCTTTTATATACTAAGTTGGCAATATAAAAAAGCA 178
Db 1763 TATATCATTTTACGTTTCTCGTTCAGCTTTTATATACTAAGTTGGCAATATAAAAAAGCA 1822

QY 179 TTGCTTATCAATTTGTTGCAACGACGTCACCTATCAGTCAAAATCAATTTAATATGATATT 238
Db 1823 TTGCTTATCAATTTGTTGCAACGACGTCACCTATCAGTCAAAATCAATTTAATATGATATT 1882

QY 239 ATTTC 243
Db 1883 ATTTC 1887

RESULT 12
US-10-270-176-13
; Sequence 13, Application US/10270176
; Publication No. US20040033608A1
; GENERAL INFORMATION:
; APPLICANT: Wanner, Barry
; APPLICANT: Haldemann, Andreas
; TITLE OF INVENTION: PLASMIDS, STRAINS, AND METHODS OF USE
; FILE REFERENCE: 290.00140101
; CURRENT APPLICATION NUMBER: US/10/270,176
; CURRENT FILING DATE: 2002-10-10
; PRIOR APPLICATION NUMBER: 60/328,642
; PRIOR FILING DATE: 2001-10-10
; PRIOR APPLICATION NUMBER: 60/375,059
; PRIOR FILING DATE: 2002-04-24
; NUMBER OF SEQ ID NOS: 118
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 13
; LENGTH: 3695
; TYPE: DNA
; ORGANISM: artificial
; FEATURE:
; OTHER INFORMATION: CRIM plasmid
US-10-270-176-13

Query Match      95.1%; Score 231; DB 13; Length 3695;
Best Local Similarity 99.2%; Pred. No. 7.1e-38;
Matches 243; Conservative 0; Mismatches 0; Indels 2; Gaps 1;

QY 1 TCTGTTACAGGTCACCTAATACCATCTTAAGTAGTTCATAGTACGACTGC--ATATGTTG 58
Db 1675 TCTGTTACAGGTCACCTAATACCATCTTAAGTAGTTCATAGTACGACTGCATATATGTTG 1734

QY 59 TGTGTTACAGTATTATGTAAGTCTGTTTTTATGCAAAATCTAATTTAATATATGATATT 118
Db 1735 TGTGTTACAGTATTATGTAAGTCTGTTTTTATGCAAAATCTAATTTAATATATGATATT 1794

QY 119 TATATCATTTTACGTTTCTCGTTCAGCTTTTATATACTAAGTTGGCAATATAAAAAAGCA 178
Db 1795 TATATCATTTTACGTTTCTCGTTCAGCTTTTATATACTAAGTTGGCAATATAAAAAAGCA 1854

QY 179 TTGCTTATCAATTTGTTGCAACGACGTCACCTATCAGTCAAAATCAATTTAATATGATATT 238
Db 1855 TTGCTTATCAATTTGTTGCAACGACGTCACCTATCAGTCAAAATCAATTTAATATGATATT 1914

QY 239 ATTTC 243
Db 1915 ATTTC 1919

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FEATURE:
; OTHER INFORMATION: CRIM plasmid
US-10-270-176-41

Query Match 95.1%; Score 231; DB 13; Length 5646;
Best Local Similarity 99.2%; Pred. No. 8.1e-38;
Matches 243; Conservative 0; Mismatches 0; Indels 2; Gaps 1;

QY 1 TCTGTTACAGGTCACCTAATACCATCTAAGTAGTCTGATTCATCATAGTGACTGC--ATATGTTG 58
Db 3968 TCTGTTACAGGTCACCTAATACCATCTAAGTAGTCTGATTCATCATAGTGACTGCATATATGTTG 4027

QY 59 TGTGTTACAGTATTAATAGTAGTCTGTTTTTATGCAAAATCTAATTAATATATGATATT 118
Db 4028 TGTGTTACAGTATTAATAGTAGTCTGTTTTTATGCAAAATCTAATTAATATATGATATT 4087

QY 119 TATATCATTTTACGTTTCTCGTTACGCTTTTTTATACCTAAGTTGGCATTATAAAAGCA 178
Db 4088 TATATCATTTTACGTTTCTCGTTACGCTTTTTTATACCTAAGTTGGCATTATAAAAGCA 4147

QY 179 TTGCTTATCAATTTGTTGCAACGACAGTCACTATCAGTCAAAATATAATCATTTATTG 238
Db 4148 TTGCTTATCAATTTGTTGCAACGACAGTCACTATCAGTCAAAATATAATCATTTATTG 4207

QY 239 ATTTC 243
Db 4208 ATTTC 4212

RESULT 15
US-10-270-176-40
; Sequence 40, Application US/10270176
; Publication No. US20040033608A1
; GENERAL INFORMATION:
; APPLICANT: Wanner, Barry
; APPLICANT: Haldmann, Andreas
; TITLE OF INVENTION: PLASMIDS, STRAINS, AND METHODS OF USE
; FILE REFERENCE: 290.00140101
; CURRENT APPLICATION NUMBER: US/10/270,176
; CURRENT FILING DATE: 2002-10-10
; PRIOR APPLICATION NUMBER: 60/328,642
; PRIOR FILING DATE: 2001-10-10
; PRIOR APPLICATION NUMBER: 60/375,059
; PRIOR FILING DATE: 2002-04-24
; NUMBER OF SEQ ID NOS: 118
; SOFTWARE: Patent in version 3.0
; SEQ ID NO 40
; LENGTH: 5706
; TYPE: DNA
; ORGANISM: artificial
; FEATURE:
; OTHER INFORMATION: CRIM plasmid
US-10-270-176-40

Query Match 95.1%; Score 231; DB 13; Length 5706;
Best Local Similarity 99.2%; Pred. No. 8.1e-38;
Matches 243; Conservative 0; Mismatches 0; Indels 2; Gaps 1;

QY 1 TCTGTTACAGGTCACCTAATACCATCTAAGTAGTCTGATTCATCATAGTGACTGC--ATATGTTG 58
Db 3968 TCTGTTACAGGTCACCTAATACCATCTAAGTAGTCTGATTCATCATAGTGACTGCATATATGTTG 4027

QY 59 TGTGTTACAGTATTAATAGTAGTCTGTTTTTATGCAAAATCTAATTAATATATGATATT 118
Db 4028 TGTGTTACAGTATTAATAGTAGTCTGTTTTTATGCAAAATCTAATTAATATATGATATT 4087

QY 119 TATATCATTTTACGTTTCTCGTTACGCTTTTTTATACCTAAGTTGGCATTATAAAAGCA 178
Db 4088 TATATCATTTTACGTTTCTCGTTACGCTTTTTTATACCTAAGTTGGCATTATAAAAGCA 4147

QY 179 TTGCTTATCAATTTGTTGCAACGACAGTCACTATCAGTCAAAATATAATCATTTATTG 238
Db 4148 TTGCTTATCAATTTGTTGCAACGACAGTCACTATCAGTCAAAATATAATCATTTATTG 4207

US-10-270-176-20

RESULT 13
US-10-270-176-20
; Sequence 20, Application US/10270176
; Publication No. US20040033608A1
; GENERAL INFORMATION:
; APPLICANT: Wanner, Barry
; APPLICANT: Haldmann, Andreas
; TITLE OF INVENTION: PLASMIDS, STRAINS, AND METHODS OF USE
; FILE REFERENCE: 290.00140101
; CURRENT APPLICATION NUMBER: US/10/270,176
; CURRENT FILING DATE: 2002-10-10
; PRIOR APPLICATION NUMBER: 60/328,642
; PRIOR FILING DATE: 2001-10-10
; PRIOR APPLICATION NUMBER: 60/375,059
; PRIOR FILING DATE: 2002-04-24
; NUMBER OF SEQ ID NOS: 118
; SOFTWARE: Patent in version 3.0
; SEQ ID NO 20
; LENGTH: 4782
; TYPE: DNA
; ORGANISM: artificial
; FEATURE:
; OTHER INFORMATION: CRIM plasmid
US-10-270-176-20

Query Match 95.1%; Score 231; DB 13; Length 4782;
Best Local Similarity 99.2%; Pred. No. 7.7e-38;
Matches 243; Conservative 0; Mismatches 0; Indels 2; Gaps 1;

QY 1 TCTGTTACAGGTCACCTAATACCATCTAAGTAGTCTGATTCATCATAGTGACTGC--ATATGTTG 58
Db 2688 TCTGTTACAGGTCACCTAATACCATCTAAGTAGTCTGATTCATCATAGTGACTGCATATATGTTG 2747

QY 59 TGTGTTACAGTATTAATAGTAGTCTGTTTTTATGCAAAATCTAATTAATATATGATATT 118
Db 2748 TGTGTTACAGTATTAATAGTAGTCTGTTTTTATGCAAAATCTAATTAATATATGATATT 2807

QY 119 TATATCATTTTACGTTTCTCGTTACGCTTTTTTATACCTAAGTTGGCATTATAAAAGCA 178
Db 2808 TATATCATTTTACGTTTCTCGTTACGCTTTTTTATACCTAAGTTGGCATTATAAAAGCA 2867

QY 179 TTGCTTATCAATTTGTTGCAACGACAGTCACTATCAGTCAAAATATAATCATTTATTG 238
Db 2868 TTGCTTATCAATTTGTTGCAACGACAGTCACTATCAGTCAAAATATAATCATTTATTG 2927

QY 239 ATTTC 243
Db 2928 ATTTC 2932

RESULT 14
US-10-270-176-41
; Sequence 41, Application US/10270176
; Publication No. US20040033608A1
; GENERAL INFORMATION:
; APPLICANT: Wanner, Barry
; APPLICANT: Haldmann, Andreas
; TITLE OF INVENTION: PLASMIDS, STRAINS, AND METHODS OF USE
; FILE REFERENCE: 290.00140101
; CURRENT APPLICATION NUMBER: US/10/270,176
; CURRENT FILING DATE: 2002-10-10
; PRIOR APPLICATION NUMBER: 60/328,642
; PRIOR FILING DATE: 2001-10-10
; PRIOR APPLICATION NUMBER: 60/375,059
; PRIOR FILING DATE: 2002-04-24
; NUMBER OF SEQ ID NOS: 118
; SOFTWARE: Patent in version 3.0
; SEQ ID NO 41
; LENGTH: 5646
; TYPE: DNA
; ORGANISM: artificial

QY 239 ATTTC 243
|||
Db 4208 ATTTC 4212

Search completed: September 10, 2004, 00:14:07
Job time : 307.981 secs

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(without alignments)
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Title: US-10-082-772B-3
Perfect score: 102
Sequence: 1 ctgcttttttataactaagtt.....taaaatcattattgatttc 102

Scoring table: IDENTITY_NUC
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Maximum Match 100%
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- 40: em_htgo_mus.*
- 41: em_htgo_other.*

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score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
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4	102	100.0	1421	10	AF121976	AF121976 Mus muscu
5	102	100.0	2408	6	AR059581	AR059581 Sequence
6	102	100.0	2408	6	AR063063	AR063063 Sequence
7	102	100.0	2408	6	I93548	I93548 Sequence 69
8	102	100.0	2408	6	AR370418	AR370418 Sequence
9	102	100.0	3049	6	AX430197	AX430197 Sequence
10	102	100.0	3049	6	AX449167	AX449167 Sequence
11	102	100.0	3111	8	CPFERAS	X52304 Chlamydomon
12	102	100.0	3484	6	A51914	A51914 Sequence 1
13	102	100.0	3484	6	AR309120	AR309120 Sequence
14	102	100.0	3484	6	AR372694	AR372694 Sequence
15	102	100.0	3484	6	BD007602	BD007602 Nematoda-
16	102	100.0	3757	6	AR080463	AR080463 Sequence
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18	102	100.0	5349	6	A71437	A71437 Sequence 7
19	102	100.0	5349	6	AR207455	AR207455 Sequence
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21	102	100.0	5611	6	A71440	A71440 Sequence 10
22	102	100.0	5611	6	AR207458	AR207458 Sequence
23	102	100.0	5611	6	BD069514	BD069514 Improved
24	102	100.0	6803	8	AB069968	AB069968 Oryza sat
25	102	100.0	9819	8	ZMA428542	AJ428542 Zea mays
26	102	100.0	9918	1	AE005255	AE005255 Escherich
27	102	100.0	297816	1	AP002553	AP002553 Escherich
28	101	99.0	2934	3	TRGP85B	M91470 Trypanosoma
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32	100.4	98.4	201	6	I36498	I36498 Sequence 18
33	100.4	98.4	243	6	AX092113	AX092113 Sequence
34	100.4	98.4	361	7	LAMINTATT	M23841 Bacterioph
35	100.4	98.4	610	6	AX101000	AX101000 Sequence
36	100.4	98.4	1668	9	NACHRS	D85521 Macaca fasc
37	100.4	98.4	1763	6	BD225932	BD225932 Immediate
38	100.4	98.4	2758	3	PFAHRPC	M17028 P.falciparu
39	100.4	98.4	2959	12	AY048723	AY048723 CRIM plas
40	100.4	98.4	3485	12	AF178449	AF178449 Integrati
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43	100.4	98.4	3695	12	AY048733	AY048733 CRIM plas
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45	100.4	98.4	4190	12	XXU13848	U13848 pExCell Clo

ALIGNMENTS

RESULT 1
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LOCUS AX092114 102 bp DNA linear PAT 21-MAR-2001
DEFINITION Sequence 3 from Patent WO0116345.
ACCESSION AX092114
VERSION AX092114.1 GI:13444357
KEYWORDS
SOURCE Escherichia coli
ORGANISM Escherichia coli
REFERENCE 1
AUTHORS Drooge, P.
TITLE Sequence-specific dna recombination in eukaryotic cells
JOURNAL Patent: WO 0116345-A 3 08-MAR-2001;
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Escherichia.

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      /mol_type="unassigned DNA"
      /db_xref="taxon:562"
ORIGIN
  Query Match      100.0%; Score 102; DB 6; Length 102;
  Best Local Similarity 100.0%; Pred. No. 1.1e-14;
  Matches 102; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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  HUMDTN02
  LOCUS      HUMDTN02      979 bp DNA linear PRI 21-NOV-2001
  DEFINITION Human dystrobrevin (DTN) gene, exon 2.
  ACCESSION U84530
  VERSION U84530.1 GI:2149295
  KEYWORDS
  SEGMENT
  SOURCE
  ORGANISM
    Homo sapiens (human)
    Homo sapiens
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
  1 (bases 1 to 979)
  Sadoulet-Puccio,H.M., Feener,C.A., Schaid,D.J., Thibodeau,S.N.,
  Michels,V.V. and Kunkel,L.M.
  The genomic organization of human dystrobrevin
  Neurogenetics 1 (1), 37-42 (1997)
  20197320
  10735273
  2 (bases 1 to 979)
  Sadoulet-Puccio,H.M., Feener,C.A. and Kunkel,L.M.
  Direct Submission
  Submitted (09-JAN-1997) Genetics, HHMI, 320 Longwood Avenue,
  Boston, MA 02115, USA
  Location/Qualifiers
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    /chromosome="18"
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  QY 61 AACAGTCTACTATCAGTCAAAATAAAATCATATTATTGATTC 102
  Db 143 AACAGTCTACTATCAGTCAAAATAAAATCATATTATTGATTC 184
  RESULT 3
  HSA325746/c
  LOCUS      HSA325746      1090 bp DNA linear PRI 18-JUL-2002
  DEFINITION Homo sapiens genomic sequence surrounding NotI site, clone
  ACCESSION NBI-850S.
  VERSION AJ325746.1 GI:15870140
  KEYWORDS
  SOURCE
  ORGANISM
    Homo sapiens (human)
    Homo sapiens
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
  1 (bases 1 to 1090)
  Kutsenko,A.S., Gizatullin,R.Z., Al-Amin,A.N., Wang,F., Kvasha,S.M.,
  Podewski,R.M., Matushkin,Y.G., Gyanchandani,A., Muravenko,O.V.,
  Levitsky,V.G., Kolchanov,N.A., Protodopov,A.I., Kashuba,V.I.,
  Kisselev,L.L., Wasserman,W., Wahlestedt,C. and Zabarovsky,E.R.
  NotI flanking sequences: a tool for gene discovery and verification
  of the human genome
  Nucleic Acids Res. 30 (14), 3163-3170 (2002).
  Nucleic Acids Res. 30 (14), 3163-3170 (2002).
  MEDLINE 22131767
  PUBMED 12136098
  REFERENCE
  AUTHORS Zabarovsky,E.R.
  DIRECT SUBMISSION
  TITLE Submitted (16-MAY-2001) Microbiology and Tumorbiology Centre,
  Karolinska Institute, Theorells vag, 3, Box 280, Stockholm 171 77,
  Sweden
  Location/Qualifiers
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  QY 61 AACAGTCTACTATCAGTCAAAATAAAATCATATTATTGATTC 102
  Db 204 AACAGTCTACTATCAGTCAAAATAAAATCATATTATTGATTC 163
  RESULT 4
  AF121976
  LOCUS      AF121976      1421 bp DNA linear ROD 07-DEC-1999
  DEFINITION Mus musculus odorant receptor S19 gene, complete cds.
  ACCESSION AF121976
  VERSION AF121976.2 GI:6532000
  KEYWORDS
  SOURCE
  ORGANISM
    Mus musculus (house mouse)
    Mus musculus
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
  1 (bases 442 to 1421)
  Malnic,B., Hirono,J., Sato,T. and Buck,L.B.
  Combinatorial receptor codes for odors
  Cell 96 (5), 713-723 (1999)
  99189756
  10089886
  2 (bases 442 to 1421)
  Malnic,B., Hirono,J., Sato,T. and Buck,L.B.
  Direct Submission
  TITLE Submitted (20-JAN-1999) Neurobiology, Harvard Medical School, 220
  Longwood Avenue, Boston, MA 02115, USA
  JOURNAL
  MEDLINE 99189756
  PUBMED 10089886
  REFERENCE
  AUTHORS Malnic,B., Hirono,J., Sato,T. and Buck,L.B.
  TITLE Submitted (07-DEC-1999) Neurobiology, Harvard Medical School, 220
  Longwood Avenue, Boston, MA 02115, USA
  JOURNAL
  MEDLINE 99189756
  PUBMED 10089886
  REFERENCE
  AUTHORS Malnic,B., Hirono,J., Sato,T. and Buck,L.B.
  TITLE Submitted (07-DEC-1999) Neurobiology, Harvard Medical School, 220
  Longwood Avenue, Boston, MA 02115, USA
  JOURNAL

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REMARK Sequence update by submitter
COMMENT On Dec 7, 1999 this sequence version replaced gi:4680261.

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/note="G-protein-coupled receptor"
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/product="odorant receptor S19"
/protein_id="AAD27596.2"
/db_xref="GI:6532001"
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STLLPKMLAIFWLRSHVISYHGLCTQMFVHAFATSAVILLAMAFDRVATCRPLHY
TSILNAVIGIKGLACVTGGLLFVFPVILIERLPCGHHIIPHTYCEHMGIAKLACA
SIKPNITVGLTVALSVTGMVDVYLATSYLILQAVLRPSKDAQFRAFSTCGAHICVI
LVFYIPAFESFTFRGHVPPQVHHILANLYLLVPPVLPVLPVYGINTKQIRLILDF
FVKR"

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Query Match 100.0%; Score 102; DB 10; Length 1421;
Best Local Similarity 100.0%; Pred. No. 1e-14; Mismatches 0; Indels 0; Gaps 0;
Matches 102; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 129 CTGCTTTTATCTAAGTTGGCAATATAAAAGCAATGCTTATCAATTTGTTGCAACG 188
QY 61 AACAGGTCACATCATCAAGTCAAAATAAATCAATTTGATTTC 102
Db 189 AACAGGTCACATCATCAAGTCAAAATAAATCAATTTGATTTC 230

RESULT 5

AR059581
LOCUS AR059581 2408 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 69 from patent US 5840498.
ACCESSION AR059581
VERSION AR059581.1 GI:5986031
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 2408)
AUTHORS Selsted,M.E. and Ouellette,A.J.
TITLE Antibiotic cryptidin peptides and methods of their use
JOURNAL Patent: US 5840498-A 69 24-NOV-1998;
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ORIGIN

Query Match 100.0%; Score 102; DB 6; Length 2408;
Best Local Similarity 100.0%; Pred. No. 9.4e-15; Mismatches 0; Indels 0; Gaps 0;
Matches 102; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 408 CTGCTTTTATCTAAGTTGGCAATATAAAAGCAATGCTTATCAATTTGTTGCAACG 467
QY 61 AACAGGTCACATCATCAAGTCAAAATAAATCAATTTGATTTC 102
Db 468 AACAGGTCACATCATCAAGTCAAAATAAATCAATTTGATTTC 509

RESULT 6

AR063063
LOCUS AR063063 2408 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 69 from patent US 5844072.
ACCESSION AR063063
VERSION AR063063.1 GI:5990754
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 2408)
AUTHORS Selsted,M.E. and Ouellette,A.J.
TITLE Antibiotic cryptidin peptides and methods of their use
JOURNAL Patent: US 5844072-A 69 01-DEC-1998;
FEATURES
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1..2408
/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN

Query Match 100.0%; Score 102; DB 6; Length 2408;
Best Local Similarity 100.0%; Pred. No. 9.4e-15; Mismatches 0; Indels 0; Gaps 0;
Matches 102; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CTGCTTTTATCTAAGTTGGCAATATAAAAGCAATGCTTATCAATTTGTTGCAACG 60
Db 408 CTGCTTTTATCTAAGTTGGCAATATAAAAGCAATGCTTATCAATTTGTTGCAACG 467
QY 61 AACAGGTCACATCATCAAGTCAAAATAAATCAATTTGATTTC 102
Db 468 AACAGGTCACATCATCAAGTCAAAATAAATCAATTTGATTTC 509

RESULT 7

AR063063
LOCUS AR063063 2408 bp DNA linear PAT 01-DEC-1998
DEFINITION Sequence 69 from patent US 5731149.
ACCESSION AR063063
VERSION AR063063.1 GI:3938018
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 2408)
AUTHORS Selsted,M.E. and Ouellette,A.J.
TITLE Antibiotic cryptidin peptides and methods of their use
JOURNAL Patent: US 5731149-A 69 24-MAR-1998;
FEATURES
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Matches 102; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 408 CTGCTTTTATCTAAGTTGGCAATATAAAAGCAATGCTTATCAATTTGTTGCAACG 467
QY 61 AACAGGTCACATCATCAAGTCAAAATAAATCAATTTGATTTC 102
Db 468 AACAGGTCACATCATCAAGTCAAAATAAATCAATTTGATTTC 509

RESULT 8

AR370418
LOCUS AR370418 2408 bp DNA linear PAT 12-SEP-2003
DEFINITION Sequence 69 from patent US 6300470.
ACCESSION AR370418
VERSION AR370418.1 GI:34606949
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.

Fri Sep 10 09:49:25 2004

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Unclassified.
REFERENCE 1 (bases 1 to 2408)
AUTHORS Selsted,M.B. and Ouellette,A.J.
TITLE Antibiotic cryptidin peptides and methods of their use
JOURNAL Patent: US 6300470-A 69 09-OCT-2001;
FEATURES
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Query Match 100.0%; Score 102; DB 6; Length 2408;
Best Local Similarity 100.0%; Pred. No. 9.4e-15;
Matches 102; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 61 AACAGTCTACTATCAGTCAAAATATAAATCAATTATTGATTTC 102
Db 468 AACAGTCTACTATCAGTCAAAATATAAATCAATTATTGATTTC 509
RESULT 9
AX430197 3049 bp DNA linear PAT 28-JUN-2002
DEFINITION Sequence 4 from Patent EP1207204.
ACCESSION AX430197
VERSION AX430197.1 GI:21655562
SOURCE Beta vulgaris
ORGANISM Beta vulgaris
REFERENCE 1
AUTHORS Hehl,R., Kloos,D. and Stahl,D.J.
TITLE Tissue-specific promoters from sugar beet
JOURNAL Patent: Ep 1207204-A 4 22-MAY-2002;
KWS Saat AG (DE)
FEATURES
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    1..3049
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    mRNA 2928..3049
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Best Local Similarity 100.0%; Pred. No. 9e-15;
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Db 408 CTGCTTTTATCTAAGTTGGCATTATATAAAGCATTGCTTATCAATTGTTGCAACG 467
QY 61 AACAGTCTACTATCAGTCAAAATATAAATCAATTATTGATTTC 102
Db 468 AACAGTCTACTATCAGTCAAAATATAAATCAATTATTGATTTC 509
RESULT 11
CRPERAS 3111 bp mRNA linear PLN 23-MAR-1995
LOCUS Chlamydomonas mRNA for periplasmic arylsulfatase.
DEFINITION X52304
ACCESSION X52304
VERSION X52304.1 GI:18173
KEYWORDS arylsulfatase; AS gene; periplasmic protein.
SOURCE Chlamydomonas reinhardtii
ORGANISM Chlamydomonas reinhardtii
REFERENCE 1 (bases 481 to 3111)
AUTHORS de Hostos,E.L., Schilling,J. and Grossman,A.R.
TITLE Structure and expression of the gene encoding the periplasmic arylsulfatase of Chlamydomonas reinhardtii
JOURNAL Mol. Gen. Genet. 218 (2), 229-239 (1989)
MEDLINE 89384447
PUBMED 2476654
REFERENCE 2 (bases 1 to 3111)
AUTHORS de Hostos,E.L.
TITLE Direct Submission
JOURNAL Submitted (11-APR-1990) De Hostos E.L., Max-Planck-Institute for Biochemistry, Am Klopferspitz 18A, 8033 Martinsried, FRG
COMMENT The sequence is a composite of a cDNA (for CDS region) and genomic. See <X16179> for intron between bases 717-718. See <X16180> for bases 616-3104.
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Matches 102; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTGCTTTTATACTAAGTGGCATTATATAAAAGCATTGCTTATCAATTGTTGCAACG 60
DB 72 CTGCTTTTATACTAAGTGGCATTATATAAAAGCATTGCTTATCAATTGTTGCAACG 131
QY 61 AACAGGTCACATCATCAGTCACAAATAAAATCAATATTGATTTC 102
DB 132 AACAGGTCACATCATCAGTCACAAATAAAATCAATATTGATTTC 173

RESULT 12
A91914
LOCUS 3484 bp DNA linear PAT 22-JAN-2000
DEFINITION Sequence 1 from Patent WO9822599.
ACCESSION A91914
VERSION A91914.1 GI:6740781
SOURCE Arabidopsis thaliana (thale cress)
ORGANISM Arabidopsis thaliana
AUTHORS Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsi.
1 (bases 1 to 3484)
OHl,S.A. and Klap,J.
TITLE NEMATODE-INDUCIBLE REGULATORY DNA SEQUENCES
JOURNAL Patent: WO 9822599-A 1 28-MAY-1998;
LEE FREDERIQUE MARTANNE V D (NL); OHL STEPHAN ANDREAS (NL)
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Query Match 100.0%; Score 102; DB 6; Length 3484;
Best Local Similarity 100.0%; Pred. No. 8.8e-15;
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QY 1 CTGCTTTTATACTAAGTGGCATTATATAAAAGCATTGCTTATCAATTGTTGCAACG 60
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RESULT 14
AR372694
LOCUS 3484 bp DNA linear PAT 12-SEP-2003
DEFINITION Sequence 1 from patent US 6395963.
ACCESSION AR372694
VERSION AR372694.1 GI:34610045
KEYWORDS
SOURCE
ORGANISM
Unclassified.
1 (bases 1 to 3484)
OHl,S.A., Sijmons,P.C., Klein-Van der Lee,F.M., Goddijn,O. and
Klap,J.
TITLE Nematode-inducible regulatory DNA sequences
JOURNAL Patent: US 6395963-A 1 28-MAY-2002;
Location/Qualifiers
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Best Local Similarity 100.0%; Pred. No. 8.8e-15;
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DB 420 CTGCTTTTATACTAAGTGGCATTATATAAAAGCATTGCTTATCAATTGTTGCAACG 479

RESULT 14
AR372694
LOCUS 3484 bp DNA linear PAT 12-SEP-2003
DEFINITION Sequence 1 from patent US 6395963.
ACCESSION AR372694
VERSION AR372694.1 GI:34610045
KEYWORDS
SOURCE
ORGANISM
Unclassified.
1 (bases 1 to 3484)
OHl,S.A., Sijmons,P.C., Klein-Van der Lee,F.M., Goddijn,O. and
Klap,J.
TITLE Nematode-inducible regulatory DNA sequences
JOURNAL Patent: US 6395963-A 1 28-MAY-2002;
Location/Qualifiers
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ORIGIN
Query Match 100.0%; Score 102; DB 6; Length 3484;
Best Local Similarity 100.0%; Pred. No. 8.8e-15;
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Query Match 100.0%; Score 102; DB 6; Length 3484;
Best Local Similarity 100.0%; Pred. No. 8.8e-15;
Matches 102; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTGCTTTTATACTAAGTGGCATTATATAAAAGCATTGCTTATCAATTGTTGCAACG 60
DB 420 CTGCTTTTATACTAAGTGGCATTATATAAAAGCATTGCTTATCAATTGTTGCAACG 479

RESULT 13
AR309120
LOCUS 3484 bp DNA linear PAT 12-JUN-2003
DEFINITION Sequence 1 from patent US 6555529.
ACCESSION AR309120
VERSION AR309120.1 GI:31700962
KEYWORDS
SOURCE
Unknown.
ORGANISM
Unknown.
Unclassified.
1 (bases 1 to 3484)
Funaba,Y., Koike,J., Tanahashi,M., Okazaki,S. and Ito,M.
Remedies for intramedullary diseases
Patent: US 6555529-A 1 29-APR-2003;
Location/Qualifiers
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ORIGIN
Query Match 100.0%; Score 102; DB 6; Length 3484;
Best Local Similarity 100.0%; Pred. No. 8.8e-15;
Matches 102; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTGCTTTTATACTAAGTGGCATTATATAAAAGCATTGCTTATCAATTGTTGCAACG 60
DB 420 CTGCTTTTATACTAAGTGGCATTATATAAAAGCATTGCTTATCAATTGTTGCAACG 479

RESULT 14
AR372694
LOCUS 3484 bp DNA linear PAT 12-SEP-2003
DEFINITION Sequence 1 from patent US 6395963.
ACCESSION AR372694
VERSION AR372694.1 GI:34610045
KEYWORDS
SOURCE
ORGANISM
Unclassified.
1 (bases 1 to 3484)
OHl,S.A., Sijmons,P.C., Klein-Van der Lee,F.M., Goddijn,O. and
Klap,J.
TITLE Nematode-inducible regulatory DNA sequences
JOURNAL Patent: US 6395963-A 1 28-MAY-2002;
Location/Qualifiers
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/organism="unknown"
/mol_type="genomic DNA"

ORIGIN
Query Match 100.0%; Score 102; DB 6; Length 3484;
Best Local Similarity 100.0%; Pred. No. 8.8e-15;
Matches 102; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTGCTTTTATACTAAGTGGCATTATATAAAAGCATTGCTTATCAATTGTTGCAACG 60
DB 420 CTGCTTTTATACTAAGTGGCATTATATAAAAGCATTGCTTATCAATTGTTGCAACG 479

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Db 420 CTGCTTTTATATACTAAGTTGGCATTATATAAAAGCATTGCTTATCATCAATTGTTGCAACG 479

Qy 61 AACAGGTCACATCAAGTCAAAATAAAATCAATTATTGATTTC 102
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Db 480 AACAGGTCACATCAAGTCAAAATAAAATCAATTATTGATTTC 521

RESULT 15
BD007602
LOCUS BD007602 3484 bp DNA linear PAT 31-JAN-2002
DEFINITION Nematoda-induced regulatory DNA sequence.
ACCESSION BD007602
VERSION BD007602.1 GI:18635975
KEYWORDS JP 2001503992-A/1.
SOURCE Arabidopsis thaliana (thale cress)
ORGANISM Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsi.
REFERENCE 1 (bases 1 to 3484)
AUTHORS Andreas,S., Lee,F.M.V.D., Goddijn,O.J.M., Klap,J. and Simons,P.C.
TITLE Nematoda-induced regulatory DNA sequence
JOURNAL Patent: JP 2001503992-A 1 27-MAR-2001;
MOHEN INTERNATIONAL NV
COMMENT OS Arabidopsis thaliana (thale cress)
PN JP 2001503992-A/1
PD 27-MAR-2001
PF 18-NOV-1997 JP 1998523219
PR 18-NOV-1996 EP 96203213.2
PI STEPHEN ANDREAS,FREDERIQUE MARIANNE VAN DER LEE, PI OSCAR
JOHANNES MARIA GODDIJN,JOKE KLAP,PETER CHRISTIAN SIMONS PC
C12N15/09,A01H5/00,A01N65/00,C12N1/15,C12N1/19,C12N1/21, PC
C12N5/10,C12N9/22,
PC C12N15/00,C12N5/00
CC Strandedness: Double;
CC Topology: Linear;
FH Key Location/Qualifiers
FT CDS 3481..3484.
source Location/Qualifiers
1..3484
/organism="Arabidopsis thaliana"
/mol_type="genomic DNA"
/db_xref="taxon:3702"

ORIGIN

Query Match 100.0%; Score 102; DB 6; Length 3484;
Best Local Similarity 100.0%; Pred. No. 8.8e-15;
Matches 102; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTGCTTTTATATACTAAGTTGGCATTATATAAAAGCATTGCTTATCATCAATTGTTGCAACG 60
|||||
Db 420 CTGCTTTTATATACTAAGTTGGCATTATATAAAAGCATTGCTTATCATCAATTGTTGCAACG 479

Qy 61 AACAGGTCACATCAAGTCAAAATAAAATCAATTATTGATTTC 102
|||||
Db 480 AACAGGTCACATCAAGTCAAAATAAAATCAATTATTGATTTC 521

Search completed: September 9, 2004, 19:34:31
Job time : 706.078 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: September 9, 2004, 13:30:05 : Search time 116.156 Seconds
(without alignments)
3730.479 Million cell updates/sec

Title: US-10-082-772B-3

Perfect score: 102

Sequence: 1 ctgctttttataactaagtt.....taaaatcattatttgatttc 102

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 3373863 seqs, 2124099041 residues

Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

N Geneseq_29Jan04.*

1: Geneseqn1980s.*

2: Geneseqn1990s.*

3: Geneseqn2000s.*

4: Geneseqn2001as.*

5: Geneseqn2001bs.*

6: Geneseqn2002s.*

7: Geneseqn2003as.*

8: Geneseqn2003bs.*

9: Geneseqn2003cs.*

10: Geneseqn2004s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB ID	Description
1	102	100.0	102	4	Aaf61419 E. coli a
2	102	100.0	2408	2	AAT30737 Rat crypt
3	102	100.0	3049	6	ABN81284 Beet prom
4	102	100.0	3484	2	AAV34987 Arabidops
5	102	100.0	3757	2	AAV44332 Murine mm
6	102	100.0	3757	2	AAV42708 Mouse mas
7	102	100.0	5349	2	AAV23239 T-DNA of
8	102	100.0	5611	2	AAV23242 Plasmid p
9	100.4	98.4	201	2	AAQ50319 Detection
10	100.4	98.4	243	4	Aaf61418 Bacteriop
11	100.4	98.4	248	8	ACC85316 Recombina
12	100.4	98.4	282	7	ACC44676 Murine rD
13	100.4	98.4	282	7	ABT16636 Artificia
14	100.4	98.4	610	5	AAf79770 Bacteriop
15	100.4	98.4	1469	7	ABQ80306 Lambda fr
16	100.4	98.4	1469	7	ACC83020 Bacteriop
17	100.4	98.4	1763	2	AAZ30709 Rat neuro
18	100.4	98.4	4345	7	ACC44716 Plasmid p
19	100.4	98.4	4346	7	ABT16615 Artificia
20	100.4	98.4	4909	2	AAT18924 Vector pl
21	100.4	98.4	5641	4	AAf30800 Plasmid p
22	100.4	98.4	5670	4	AAf30801 Vector pl
23	100.4	98.4	5826	4	AAf30798 Vector pl

24	100.4	98.4	6071	4	AAf30799 Vector pl
25	100.4	98.4	7652	2	AAQ45682 Sequencin
26	98.8	96.9	243	4	Aaf61421 E. coli a
27	98.4	96.5	7508	8	AAI62713 Escherich
28	93.8	92.0	100	3	AAc55386 Recombina
29	93.8	92.0	100	7	ACc55959 Nucleic a
30	93.8	92.0	2717	3	AAc55422 Entry vec
31	93.8	92.0	2717	3	AAc55437 Entry vec
32	93.8	92.0	2717	7	ABz58764 Entry vec
33	93.8	92.0	2718	3	AAc55425 Entry vec
34	93.8	92.0	2720	3	AAc55431 Entry vec
35	93.8	92.0	2720	3	AAc55434 Entry vec
36	93.8	92.0	2723	3	AAc55428 Entry vec
37	93.8	92.0	2735	3	AAc55446 Entry vec
38	93.8	92.0	2735	3	AAc55443 Entry vec
39	93.8	92.0	2738	3	AAc55449 Entry vec
40	93.8	92.0	2738	3	AAc55440 Entry vec
41	93.8	92.0	2744	3	AAc55452 Entry vec
42	92.2	90.4	659	9	ADc06860 Plasmid p
43	92.2	90.4	660	9	ADc06864 Plasmid p
44	92.2	90.4	2591	6	ABK88866 Topoisome
45	92.2	90.4	2591	10	ADe83789 Plasmid p

ALIGNMENTS

RESULT 1

AAf61419
ID AAF61419 standard; DNA; 102 BP.
XX
AC AAF61419;
XX
DT 05-JUN-2001 (first entry)
XX
DE E. coli attL DNA fragment.
XX
KW Sequence-specific recombination; SSR; integrase; gene therapy; somatic;
KW targeted integration; attL; ds.
XX
OS Escherichia coli.
XX
PN DE19941186-A1.
XX
PD 01-MAR-2001.
XX
PF 30-AUG-1999; 99DE-01041186.
XX
PR 30-AUG-1999; 99DE-01041186.
XX
FA (DROE/) DROEGE P.
XX
PI Droege P;
XX
DR WPI; 2001-246016/26.
XX

Sequence-specific recombination of DNA in eukaryotes, useful particularly for somatic cell gene therapy, uses an integrase to effect recombination between att sites.

Claim 3; Page 14; 24pp; German.

This invention describes a novel sequence-specific recombination (SSR) of DNA in a eukaryotic cell, comprising introducing two DNA sequences (I, II) into a cell, using an integrase (Int) to effect SSR. The invention also describes (1) a nucleic acid comprising a 243 base pair sequence (III), fully defined in the specification, or its derivatives; and (2) vector containing (III), or its derivatives, plus a therapeutic gene, or its derivatives. The method is particularly used in somatic gene therapy in humans and animals, but can be applied more generally for gene transfer to animal or plant cells. The method is simple and controllable, and provides stable and targeted integration of selected DNA sequences

SQ Sequence 102 BP; 35 A; 16 C; 13 G; 38 T; 0 U; 0 Other;
 Query Match 100.0%; Score 102; DB 4; Length 102;
 Best Local Similarity 100.0%; Pred. No. 4.5e-19;
 Matches 102; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTGCTTTTATACAAAGTGGCATTATATAAAAGCAATTCATCAATTTGTCACAG 60
 DB 1 CTGCTTTTATACAAAGTGGCATTATATAAAAGCAATTCATCAATTTGTCACAG 60

QY 61 AACAGTCACTATCAGTCAAAATAAAATCAATTTGATTC 102
 DB 61 AACAGTCACTATCAGTCAAAATAAAATCAATTTGATTC 102

RESULT 2
 AAT30737
 ID AAT30737 standard; DNA; 2408 BP.
 XX
 AC AAT30737;
 XX
 DT 20-OCT-1996 (first entry)
 XX
 DE Rat cryptdin 2 gene.
 XX
 KW Cryptdin 2; antibiotic; antimicrobial; defensin; inflammation;
 KW antinflammatory; inflammatory bowel disease; pancreatitis; cancer;
 KW tumour; ileitis; ds.
 XX
 OS Rattus sp.
 XX
 FH Key Location/Qualifiers
 FT exon 1. .1345
 FT /tag= a
 FT /codon_start= 1174. .1176
 FT /note= "exon 1 codes for the 5' untranslated region and
 FT cryptdin-1 prepro sequence"
 FT intron 1345. .1930
 FT /tag= b
 FT exon 1931. .2408
 FT /tag= c
 FT /note= "exon 2 codes for cryptdin-2 and 3' untranslated
 FT region"
 XX
 FN W09616075-A1.
 XX
 XX 30-MAY-1996.
 XX
 PF 05-OCT-1995; 95WO-US013328.
 XX
 XX 18-NOV-1994; 94US-00342268.
 XX
 XX (REGC) UNIV CALIFORNIA.
 PA (SHRI-) SHRINER'S HOSPITAL FOR CRIPPLED CHILDREN.
 XX
 PI Selsted ME, Ouellette AJ;
 XX
 XX WPI; 1996-268527/27.
 DR P-PSDB; AAR98787, AAR98792.
 XX
 XX New isolated cryptdin peptide(s) - which have antimicrobial activity,
 PT used partic. in the detection and treatment of inflammatory pathologies.
 XX
 PS Claim 31; Page 64-65; 103pp; English.
 XX
 CC The rat cryptdin-2 gene (T30737) codes for the precursor (R98787) of
 CC cryptdin-2 (R98792), an antimicrobial peptide that exhibits activity
 CC against a broad range of intestinal and opportunistic pathogens. Rat
 CC cryptdin-1, -2, and -3 genes (see also T30736 and T30738) were isolated
 CC from a Sprague-Dawley genomic library cloned in EMBL3. The cryptdin-2
 CC gene, or corresponding cDNA (see also T30734), can be used to produce
 CC large amounts of cryptdin-2 for use in treating inflammatory pathologies
 CC of the intestine

XX
 SQ Sequence 2408 BP; 640 A; 531 C; 557 G; 680 T; 0 U; 0 Other;
 Query Match 100.0%; Score 102; DB 2; Length 2408;
 Best Local Similarity 100.0%; Pred. No. 6.5e-19;
 Matches 102; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTGCTTTTATACAAAGTGGCATTATATAAAAGCAATTCATCAATTTGTCACAG 60
 DB 408 CTGCTTTTATACAAAGTGGCATTATATAAAAGCAATTCATCAATTTGTCACAG 467

QY 61 AACAGTCACTATCAGTCAAAATAAAATCAATTTGATTC 102
 DB 468 AACAGTCACTATCAGTCAAAATAAAATCAATTTGATTC 509

RESULT 3
 ABN81284
 ID ABN81284 standard; DNA; 3049 BP.
 XX
 AC ABN81284;
 XX
 DT 22-AUG-2002 (first entry)
 XX
 DE Beet promoter polynucleotide SEQ ID NO 4.
 XX
 KW Beet; promoter; carbohydrate metabolism; invertase inhibitor;
 KW fructosyl transferase; levan sucrose; nitrogen transporter protein;
 KW pathogen resistance; plant; transgenic; ds.
 XX
 OS Beta vulgaris.
 XX
 FH Key Location/Qualifiers
 FT Promoter 1. .2998
 FT /tag= a
 FT TATA_signal 2877. .2883
 FT /tag= c
 FT mRNA 2928. .3049
 FT /tag= b
 XX
 FN BP1207204-A1.
 XX
 XX 22-MAY-2002.
 XX
 PF 16-NOV-2000; 2000EP-00124989.
 XX
 PR 16-NOV-2000; 2000EP-00124989.
 XX
 PA (KWSS-) KWS SAAT AG.
 XX
 PI Hehl R, Kloos D, Stahl DJ;
 XX
 XX WPI; 2002-437465/47.
 XX
 XX New tissue-specific promoters from Beta vulgaris, useful e.g. for
 PT altering carbohydrate metabolism, express transgenes selectively in roots
 PT or aerial parts.
 XX
 PS Claim 1; Page 30-31; 57pp; German.
 XX
 CC The invention relates to a promoter (A) that is: (i) any of the sequences
 CC ABN81281-ABN81284; (ii) the complement of (i); or (iii) a sequence that
 CC hybridises to (ii). (A) are used, specifically in Beta vulgaris, to
 CC control expression of transgenes, particularly to alter carbohydrate
 CC metabolism; reduce loss of storage substances; express invertase
 CC inhibitor, fructosyl transferase, levan sucrose or genes that encode
 CC transporter proteins for nitrogen compounds, or increase resistance to,
 CC or tolerance of, pathogens. (A) provide tissue-specific transgene
 CC expression, either in roots or above-ground parts, so avoid pleiotropic
 CC effects, e.g. when expressing invertase inhibitor
 XX
 SQ Sequence 3049 BP; 783 A; 699 C; 876 G; 691 T; 0 U; 0 Other;

Query Match 100.0%; Score 102; DB 6; Length 3049;
Best Local Similarity 100.0%; Pred. No. 6.7e-19;
Matches 102; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTGCTTTTATCTAAGTTGGCATTATAAAAGACATTCCTTATCAATTGTTGCAACG 60
Db 2398 CTGCTTTTATCTAAGTTGGCATTATAAAAGACATTCCTTATCAATTGTTGCAACG 2457

QY 61 AACAGGTCATCTAGTCAGTCAAAATAAAATCATTATTGATTTC 102
Db 2458 AACAGGTCATCTAGTCAGTCAAAATAAAATCATTATTGATTTC 2499

RESULT 4
AAV34987
ID AAV34987 standard; DNA; 3484 BP.

XX
AC AAV34987;
XX
DT 17-OCT-2003 (revised)
DT 28-SEP-1998 (first entry)
XX Arabidopsis nematode feeding site-preferential promoter.

XX Promoter; nematode feeding site; root knot nematode; cyst nematode;
XX Meloidogyne incognita; Heterodera schachtii; Globodera pallida;
XX transgenic plant; pest resistance; crop protection; ds.
XX Arabidopsis thaliana; ecotype C24.

XX
FH Key Location/Qualifiers
FT CDS 3482
FT /*tag= a
FT /codon_start= 3482. .3484

XX W09822599-A1.
XX
XX 28-MAY-1998.
XX
XX 18-NOV-1997; 97WO-EP006472.
XX
XX 18-NOV-1996; 96EP-00203213.
XX
XX (MOGE-) MOGEN INT NV.
XX
XX Chl SA, Van Der Lee FW, Goddijn OJM, Klap J, Sijmons PC;
XX WPI; 1998-312484/27.

XX
XX Claim 1; Page 22-24; 47pp; English.
XX
XX This DNA fragment obtainable from Arabidopsis thaliana is capable of
XX promoting root knot and cyst nematode-inducible transcription of an
XX associated DNA sequence when reintroduced into a plant. The promoterless
XX GUS construct binary vector pMOG553 was mobilised by triparental mating
XX to Agrobacterium tumefaciens MOG101 and the resulting strain was used for
XX Arabidopsis root transformation. Line pMOG553#25 was identified as a line
XX which showed strong GUS expression inside syncytia and giant cells
XX induced by the cyst nematode Heterodera schachtii and the root knot
XX nematode Meloidogyne incognita, respectively. Promoter tags from line
XX pMOG553#25 were sequenced. The claimed DNA fragment is nematode feeding
XX site-specific. Also claimed are: (1) a portion or variant of the above
XX sequence capable of promoting root knot and cyst nematode inducible
XX transcription of an associated DNA sequence when reintroduced into a
XX plant; (2) a chimeric DNA sequence comprising a DNA fragment as above
XX plus a DNA sequence which is not naturally under its transcriptional
XX control, and which causes the production of a plant cell-disruptive
XX substance, preferably barnase; (3) a replicon comprising the chimeric DNA
XX sequence of (2), or the above DNA and at least 1 restriction endonuclease
XX recognition site; (4) a microorganism containing the replicon of (3); (5)

CC a plant cell having incorporated into its genome the chimeric DNA of (2);
CC (6) a root system of a plant consisting of the cells of (5); (7) a plant
CC consisting of the cells of (5), preferably a dicotyledonous plant,
CC especially a potato plant; (8) a plant grafted onto the root system of
CC (6); (9) a part of a plant, selected from seeds, flowers, tubers, roots,
CC leaves, fruits, pollen and wood, obtained from the plant of (7) or (8),
CC and (10) a crop consisting of the plants of (7) or (8). The DNA fragment
CC can be used to identify subfragments capable of promoting transcription
CC of an associated DNA sequence in a plant. It can also be used for making
CC hybrid regulatory DNA sequences. The chimeric DNA sequence of (2) can be
CC used for transforming plants (all claimed). The DNA sequence can be used
CC to reduce the susceptibility of a plant to parasitic nematodes. (Updated
CC on 17-OCT-2003 to standardise OS field)
XX
XX
XX Sequence 3484 BP; 1143 A; 593 C; 625 G; 1133 T; 0 U; 0 Other;
SQ
Query Match 100.0%; Score 102; DB 2; Length 3484;
Best Local Similarity 100.0%; Pred. No. 6.8e-19;
Matches 102; Conservative 0; Mismatches 0; Indels 0; Gaps 0

QY 1 CTGCTTTTATCTAAGTTGGCATTATAAAAGACATTCCTTATCAATTGTTGCAACG 60
Db 420 CTGCTTTTATCTAAGTTGGCATTATAAAAGACATTCCTTATCAATTGTTGCAACG 479

QY 61 AACAGTCATCTAGTCAGTCAAAATAAAATCATTATTGATTTC 102
Db 480 AACAGTCATCTAGTCAGTCAAAATAAAATCATTATTGATTTC 521

RESULT 5
AAV44332
ID AAV44332 standard; DNA; 3757 BP.

XX
AC AAV44332;
XX
XX 24-NOV-1998 (first entry)
XX Murine mMCP-6 zymogen gene.

XX
XX MCP-6 zymogen; mouse; mast cell protease 6; mMCP-7; tryptase-7;
XX blood clot; anticoagulant; myocardial infarction; reocclusion;
XX thromboembolism; cerebral embolism; thrombosis; therapy; ss.
XX
XX Mus sp.

XX
FH Key Location/Qualifiers
FT CDS 1803. .3098
FT /*tag= a
FT /note= "contains introns"
FT exon 1803. .1872
FT /*tag= b
FT intron 1873. .2011
FT /*tag= c
FT exon 2012. .2177
FT /*tag= d
FT intron 2178. .2297
FT /*tag= e
FT exon 2298. .2563
FT /*tag= f
FT intron 2564. .2696
FT /*tag= g
FT exon 2697. .2860
FT /*tag= h
FT intron 2861. .2933
FT /*tag= i
FT intron 2934. .3098
FT /*tag= j

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FT exon 2934..3098
FT /*tag= j
FT /number= 5
XX
XX WO9824886-A1.
XX
XX 11-JUN-1998.
XX
XX 25-NOV-1997; 97WO-US021620.
XX
XX 04-DEC-1996; 96US-0032354P.
XX
XX (BGHM ) BRIGHAM & WOMENS HOSPITAL.
XX
XX Stevens RL;
XX
XX WPI; 1998-333308/29.
XX
XX P-PSDB; AAW64242.
XX
XX New compositions containing tryptase-7, e.g. mouse mast cell protease-7 -
XX are used to treat clot formation in e.g. myocardial infarction,
XX reocclusion following angioplasty or pulmonary thrombo-embolism.
XX
XX Disclosure; Page 68-69; 92pp; English.
XX
XX This nucleotide sequence includes a coding region for mouse mast cell
XX protease 6 (mMCP-6, see AAW64242). The invention provides: compositions
XX comprising an isolated tryptase-7 (such as mMCP-7, see AAW64233); a
XX method for treating a blood clot by administering a nucleic acid molecule
XX that codes for a tryptase-7, or an expression product; a nucleic acid
XX encoding a serine protease (SP); and a method of producing a mature SP.
XX Tryptase-7 polypeptides can be used for treating disorders mediated by
XX undesirable thrombus clot formation such as myocardial infarction and
XX reocclusion following angioplasty of blood clots associated with
XX pulmonary thromboembolism, deep vein thrombosis, cerebral embolism, renal
XX vein and peripheral arterial thrombosis
XX
XX Sequence 3757 BP; 802 A; 1014 C; 1003 G; 938 T; 0 U; 0 Other;
XX
XX Query Match 100.0%; Score 102; DB 2; Length 3757;
XX Best Local Similarity 100.0%; Pred. No. 6.8e-19;
XX Matches 102; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 CTGCTTTTATACAGTTGGCATTATATAAAAGCATTGCTTATCAATTGTTGCAACG 60
XX |||||||||||||||||||||||||||||||||||||||||||||||||||||||
XX 374 CTGCTTTTATACAGTTGGCATTATATAAAAGCATTGCTTATCAATTGTTGCAACG 433
XX
XX QY 61 AACAGTCTACTATCAGTCAAAATAAAATCAATTATTGATTTC 102
XX |||||||||||||||||||||||||||||||||||||||||||||||||||||||
XX 434 AACAGTCTACTATCAGTCAAAATAAAATCAATTATTGATTTC 475
XX
XX RESULT 6
XX AAV42708
XX ID AAV42708 standard; cDNA; 3757 BP.
XX
XX AC AAV42708;
XX
XX 27-OCT-1998 (first entry)
XX
XX Mouse mast cell protease (mMCP-6) nucleic acid sequence.
XX
XX Mast cell protease; MCP; mouse; inhibitor; peptide substrate; asthma;
XX tryptase-6 protein; inflammatory disorder; allergic rhinitis; urticaria;
XX antioedema; eczematous dermatitis; atopic dermatitis; anaphylaxis;
XX hyperproliferative skin disease; peptic ulcer; hyperresponsiveness;
XX inflammatory skin condition; ss.
XX
XX Mus sp.
XX
XX WO9833812-A1.
XX
XX 06-AUG-1998.

```

```

XX 30-JAN-1998; 98WO-US001865.
XX
XX 05-FEB-1997; 97US-0037090P.
XX
XX (BGHM ) BRIGHAM & WOMENS HOSPITAL.
XX
XX Stevens RL, Huang C;
XX
XX WPI; 1998-437390/37.
XX
XX Tryptase-6 complex inhibitory peptides - used to treat mast cell-mediated
XX inflammatory disorders e.g. asthma.
XX
XX Disclosure; Page 42-43; 69pp; English.
XX
XX This represents the cDNA sequence of the mouse mast cell protease (mMCP-
XX 6). The invention provides sequences shown in AAW63160 to AAW63169 that
XX are inhibitors of mMCP-6. These peptides which are tryptase-6 complex
XX inhibitors can be used for treating a mast cell-mediated inflammatory
XX disorder. The inhibitors can be used to treat inflammatory disorders
XX including asthma, allergic rhinitis, urticaria and antioedema, eczematous
XX dermatitis (atopic dermatitis), hyperproliferative skin disease,
XX anaphylaxis, peptic ulcers, inflammatory bowel disorder,
XX hyperresponsiveness and inflammatory skin conditions
XX
XX Sequence 3757 BP; 802 A; 1014 C; 1003 G; 938 T; 0 U; 0 Other;
XX
XX Query Match 100.0%; Score 102; DB 2; Length 3757;
XX Best Local Similarity 100.0%; Pred. No. 6.8e-19;
XX Matches 102; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 CTGCTTTTATACAGTTGGCATTATATAAAAGCATTGCTTATCAATTGTTGCAACG 60
XX |||||||||||||||||||||||||||||||||||||||||||||||||||||||
XX 374 CTGCTTTTATACAGTTGGCATTATATAAAAGCATTGCTTATCAATTGTTGCAACG 433
XX
XX Db 61 AACAGTCTACTATCAGTCAAAATAAAATCAATTATTGATTTC 102
XX |||||||||||||||||||||||||||||||||||||||||||||||||||||||
XX 434 AACAGTCTACTATCAGTCAAAATAAAATCAATTATTGATTTC 475
XX
XX RESULT 7
XX AAV23239/C
XX ID AAV23239 standard; DNA; 5349 BP.
XX
XX AC AAV23239;
XX
XX 17-JUL-1998 (first entry)
XX
XX T-DNA of pTTS24.
XX
XX Barstar; barnase inhibitor; fertility restoration; male-sterile line;
XX plasmid pTTS24; T-DNA; ds.
XX
XX Synthetic.
XX
XX Key Location/Qualifiers
XX misc_feature complement(1..25)
XX /*tag= a
XX /label= RB
XX /note= "right boarder"
XX complement(98..331)
XX /*tag= b
XX /label= 3'_g7
XX /note= "region containing 3' untranslated end of
XX Agrobacterium T-DNA gene 7"
XX 332..883
XX CDS /*tag= c
XX /label= bar
XX /note= "region coding for phosphinothricin acetyl
XX transferase"
XX complement(884..2258)
XX /*tag= d
XX
XX promoter

```

```

FT      /label= P35S
FT      /note= "35S promoter of Cauliflower Mosaic Virus"
FT      2281.. .3969
FT      /tag= e
FT      /label= PE1
FT      /note= "promoter of E1 gene of rice (W09213956)"
FT      3970.. .4245
FT      /tag= f
FT      /product= "improved_barstar"
FT      4246.. .4577
FT      /tag= g
FT      /label= 3' _chs
FT      /note= "region containing 3' untranslated end of chalcone
FT      synthase gene"
FT      complement(5325.. .5349)
FT      /tag= h
FT      /note= "T-DNA left border"
FT
PN      W09810081-A2.
XX
XX      12-MAR-1998.
PD
PF      01-SEP-1997; 97WO-EP004739.
XX
XX      03-SEP-1996; 96EP-00202446.
XX
PA      (PLBZ ) PLANT GENETIC SYSTEMS NV.
XX
PI      Michiels F, Williams M;
XX      WPI; 1998-193630/17.
XX
PT      DNA encoding an improved barstar protein - used to restore fertility in
PT      male-sterile plant lines.
XX
PS      Example 4; Page 41-43; 54pp; English.
XX
CC      The present sequence was used in the preparation of an improved Bacillus
CC      amyloliquefaciens barstar, i.e. barnase inhibitor, which can be used to
CC      restore fertility to male-sterile lines. The DNA sequence encoding the
CC      improved barstar, leads to increased barstar production in tapetum cells,
CC      due to improved translation, and possibly protein stability
XX
SQ      Sequence 5349 BP; 1339 A; 1233 C; 1290 G; 1487 T; 0 U; 0 Other;
Query Match 100.0%; Score 102; DB 2; Length 5349;
Best Local Similarity 100.0%; Pred. No. 7.1e-19;
Matches 102; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy      1 CTGCTTTTATCTAAGTGGCATTATATAAAAGCATTGCTTATCAATTTGTTGCAACG 60
Db      4885 CTGCTTTTATCTAAGTGGCATTATATAAAAGCATTGCTTATCAATTTGTTGCAACG 4826
Qy      61 AACAGGTCACATCATCAGTCAAAATAAAATCAATTTATTGATTC 102
Db      4825 AACAGGTCACATCATCAGTCAAAATAAAATCAATTTATTGATTC 4784
RESULT 8
AAV23242/c
ID      AAV23242 standard; DNA; 5611 BP.
XX
AC      AAV23242;
XX
DT      17-JUL-1998 (first entry)
XX
DE      Plasmid pLH48.
XX
KW      Barstar; barnase inhibitor; fertility restoration; male-sterile line;
KW      plasmid pLH48; circular; gb.
XX
OS      Synthetic.
XX

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FH      Key
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FT      complement(39.. .317)
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FT      /label= 3' _nos
FT      /note= "region containing 3' untranslated end of nopaline
FT      synthase gene of Agrobacterium T-DA"
FT      complement(318.. .869)
FT      /tag= b
FT      /label= bar
FT      /note= "region coding for phosphinothricin acetyl
FT      transferase"
FT      complement(870.. .1702)
FT      /tag= c
FT      /label= P35S
FT      /note= "35S promoter of Cauliflower Mosaic Virus"
FT      1740.. .2284
FT      /tag= d
FT      /label= PTA29
FT      /note= "promoter of TA29 gene of Nicotiana tabacum"
FT      2285.. .2560
FT      /tag= e
FT      /product= "improved_barstar"
FT      2561.. .2892
FT      /tag= f
FT      /label= 3' _chs
FT      /note= "region containing 3' untranslated end of chalcone
FT      synthase gene"
FT
PN      W09810081-A2.
XX
XX      12-MAR-1998.
PD
PF      01-SEP-1997; 97WO-EP004739.
XX
XX      03-SEP-1996; 96EP-00202446.
XX
PA      (PLBZ ) PLANT GENETIC SYSTEMS NV.
XX
PI      Michiels F, Williams M;
XX      WPI; 1998-193630/17.
XX
PT      DNA encoding an improved barstar protein - used to restore fertility in
PT      male-sterile plant lines.
XX
PS      Disclosure; Page 45-48; 54pp; English.
XX
CC      The present sequence was used in the preparation of an improved Bacillus
CC      amyloliquefaciens barstar, i.e. barnase inhibitor, which can be used to
CC      restore fertility to male-sterile lines. The DNA sequence encoding the
CC      improved barstar, leads to increased barstar production in tapetum cells,
CC      due to improved translation, and possibly protein stability
XX
SQ      Sequence 5611 BP; 1389 A; 1342 C; 1353 G; 1527 T; 0 U; 0 Other;
Query Match 100.0%; Score 102; DB 2; Length 5611;
Best Local Similarity 100.0%; Pred. No. 7.2e-19;
Matches 102; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy      1 CTGCTTTTATCTAAGTGGCATTATATAAAAGCATTGCTTATCAATTTGTTGCAACG 60
Db      3200 CTGCTTTTATCTAAGTGGCATTATATAAAAGCATTGCTTATCAATTTGTTGCAACG 3141
Qy      61 AACAGGTCACATCATCAGTCAAAATAAAATCAATTTATTGATTC 102
Db      3140 AACAGGTCACATCATCAGTCAAAATAAAATCAATTTATTGATTC 3099
RESULT 9
AAQ50319
ID      AAQ50319 standard; DNA; 201 BP.
XX
AC      AAQ50319;

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XX 27-APR-1994 (first entry)
 XX Detection probe 11.
 XX Probe; chip; cell; detection; label; capture probe; ss.
 XX Synthetic.
 OS JP05236997-A.
 PN 17-SEP-1993.
 PD 28-FEB-1992; 92JP-00042829.
 PF 28-FEB-1992; 92JP-00042829.
 PR (HITA) HITACHI LTD.
 XX WPI; 1993-330600/42.
 XX Chip for capturing polynucleotide - has several different complementary
 PT probes fixed on cells at different sites on single tip.
 PS Disclosure; Page 8; 10pp; Japanese.
 XX The sequences given in AAQ50309-26 are probes which were used on a chip
 CC for capturing a number of target polynucleotides. A group of these probes
 CC may be attached on cells which form part of a single chip. The
 CC oligonucleotides to be detected are labelled and are complementary to the
 CC set of capture probes used. The detection chip may be used to detect a
 CC number of different polynucleotides concurrently
 XX Sequence 201 BP; 58 A; 38 C; 27 G; 78 T; 0 U; 0 Other;
 SQ Query Match 98.4%; Score 100.4; DB 2; Length 201;
 Best Local Similarity 99.0%; Pred. No. 1.3e-18;
 Matches 101; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 XX 1 CTGCTTTTATATAAGTTGGCATTATATAAAGCATTGCTTATCAATTTGTTGCAACG 60
 Db 43 CAGCTTTTATATAAGTTGGCATTATATAAAGCATTGCTTATCAATTTGTTGCAACG 102
 QY 61 AACAGTCACTATCAGTCAAAATAAATCAATTTGATTTC 102
 Db 103 AACAGTCACTATCAGTCAAAATAAATCAATTTGATTTC 144
 RESULT 10
 AAF61418
 ID AAF61418 standard; DNA; 243 BP.
 AC AAF61418;
 XX 05-JUN-2001 (first entry)
 XX Bacteriophage lambda attP DNA fragment.
 DE Sequence-specific recombination; SSR; integrase; gene therapy; somatic;
 XX targeted integration; attP; ds.
 XX Bacteriophage lambda.
 OS DE19941186-A1.
 PN 01-MAR-2001.
 PD 30-AUG-1999; 99DE-01041186.
 PF 30-AUG-1999; 99DE-01041186.
 PR (DROE/) DROEGE P.
 XX

PI Droegge P;
 XX WPI; 2001-246016/26.
 XX Sequence-specific recombination of DNA in eukaryotes, useful particularly
 PT for somatic cell gene therapy, uses an integrase to effect recombination
 PT between att sites.
 XX Claim 2; Page 13; 24pp; German.
 XX This invention describes a novel sequence-specific recombination (SSR) of
 CC DNA in a eukaryotic cell, comprising introducing two DNA sequences (I,
 CC II) into a cell, using an integrase (Int) to effect SSR. The invention
 CC also describes (1) a nucleic acid comprising a 243 base pair sequence
 CC (III), fully defined in the specification, or its derivatives; and (2)
 CC its derivatives. The method is particularly used in somatic gene therapy
 CC in humans and animals, but can be applied more generally for gene
 CC transfer to animal or plant cells. The method is simple and controllable,
 CC and provides stable and targeted integration of selected DNA sequences
 XX Sequence 243 BP; 74 A; 34 C; 33 G; 102 T; 0 U; 0 Other;
 SQ Query Match 98.4%; Score 100.4; DB 4; Length 243;
 Best Local Similarity 99.0%; Pred. No. 1.4e-18;
 Matches 101; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 CTGCTTTTATATAAGTTGGCATTATATAAAGCATTGCTTATCAATTTGTTGCAACG 60
 Db 142 CAGCTTTTATATAAGTTGGCATTATATAAAGCATTGCTTATCAATTTGTTGCAACG 201
 QY 61 AACAGTCACTATCAGTCAAAATAAATCAATTTGATTTC 102
 Db 202 AACAGTCACTATCAGTCAAAATAAATCAATTTGATTTC 243
 RESULT 11
 ACC85316
 ID ACC85316 standard; DNA; 248 BP.
 XX ACC85316;
 XX 18-SEP-2003 (first entry)
 XX Recombinase lambda integrase attP DNA recognition sequence.
 DE Vegetable plastid transformation; transgenic; recognition sequence;
 XX plant; site-specific integration; nutrition; seed production;
 KW Chemical production; ds.
 XX Unidentified.
 OS WO2003054201-A1.
 PN 03-JUL-2003.
 PD 16-DEC-2002; 2002WO-EP014303.
 PF 20-DEC-2001; 2001DE-01063159.
 PR (SUNG-) SUNGENE GMBH & CO KGAA.
 PA Biesgen C;
 PI WPI; 2003-541820/51.
 XX Site-specific integration of DNA into plastid DNA, useful for making
 PT transgenic plants used e.g. as food, by recombinase-mediated insertion.
 XX Disclosure; Page 35; 164pp; German.
 XX The present invention relates to a method for the site-specific
 CC integration of a DNA sequence into the plastid DNA of a plant or its
 CC

CC derived cells. Transgenic plants in which a DNA sequence has been
 CC integrated, also their cell cultures, organs, tissues etc. are useful in
 CC human or animal nutrition, to produce seeds, and to produce
 CC pharmaceuticals or fine chemicals, e.g. enzymes, vitamins, amino acids,
 CC flavourings and aromatizing agents, dyes, antibodies and vaccines. The
 CC present sequence is a recognition sequence shown in the exemplification
 CC of the invention
 XX
 XX Sequence 248 BP; 76 A; 35 C; 34 G; 103 T; 0 U; 0 Other;
 Query Match 98.4%; Score 100.4; DB 8; Length 248;
 Best Local Similarity 99.0%; Pred. No. 1.4e-18;
 Matches 101; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 CTGCTTTTATCTAAGTTGGCATTATAAAAAGCATTGCTTATCAATTGTTGCAACG 60
 Db 147 CAGCTTTTATCTAAGTTGGCATTATAAAAAGCATTGCTTATCAATTGTTGCAACG 206
 QY 61 AACAGGTCACATCACTCAAGTCAAAATAAATCAATCATTTGATTTC 102
 Db 207 AACAGGTCACATCACTCAAGTCAAAATAAATCAATCATTTGATTTC 248
 RESULT 12
 ACC44676
 ID ACC44676 standard; DNA; 282 BP.
 XX
 AC ACC44676;
 DT 29-MAY-2003 (first entry)
 XX
 XX Murine rDNA PCR primer SEQ ID NO:72.
 DE
 XX Chromosome-based platform; artificial chromosome; eukaryotic chromosome;
 KW att site; integrase; recombinase; ACes; gene therapy; transgenic animal;
 KW platform artificial chromosome expression system; gene; ds.
 XX
 OS Mus musculus.
 OS Synthetic.
 OS WO200297059-A2.
 PN 05-DEC-2002.
 PD
 XX 30-MAY-2002; 2002WO-US017452.
 XX
 XX 30-MAY-2001; 2001US-0294758P.
 PR 21-MAR-2002; 2002US-0366891P.
 XX
 XX (CHRO-) CHROMOS MOLECULAR SYSTEMS INC.
 PA Perkins E, Perez C, Lindenbaum M, Greene A, Leung J, Fleming E;
 PI Stewart S, Shellard J;
 PI WPI; 2003-140461/13.
 DR
 XX Novel eukaryotic chromosome comprising one or many att sites which
 PT permits site-directed integration in the presence of lambda-integrase,
 PT useful for site-specific recombination-directed integration of DNA of
 PT interest.
 XX
 XX Example 2; Page 207; 272pp; English.
 PS
 XX The present invention describes a eukaryotic chromosome (I) comprising
 CC one or several att sites, where an att site is heterologous to the
 CC chromosome, and permits site-directed integration in the presence of
 CC lambda-integrase. Also described: (1) a platform artificial chromosome
 CC expression system (ACes) (II) comprising several sites that participate
 CC in recombinase catalysed recombination; and (2) a method (M1) for
 CC introducing a heterologous nucleic acid into a platform artificial
 CC chromosome. (I) can be used in gene therapy. (M1) is useful for
 CC introducing a heterologous nucleic acid molecule into a platform
 CC artificial chromosome, preferably an ACes. (II) is useful for producing a

CC transgenic animal (e.g. a fish, insect, reptile, amphibian, arachnid, or
 CC mammal) by introducing (II) by cell fusion, lipid-mediated transfection
 CC by a carrier system, microinjection, microcell fusion, electroporation,
 CC microprojectile bombardment or direct DNA transfer into an embryonic
 CC cell, preferably a stem cell or an embryo. (II) comprises a heterologous
 CC nucleic acid that encodes a therapeutic product which is useful for
 CC making a library of ACes comprising random portions of a genome. ACC44612
 CC to ACC44732 and ABP96850 to ABP96857 represent sequences used in the
 CC exemplification of the present invention
 XX
 XX Sequence 282 BP; 79 A; 49 C; 39 G; 115 T; 0 U; 0 Other;
 Query Match 98.4%; Score 100.4; DB 7; Length 282;
 Best Local Similarity 99.0%; Pred. No. 1.4e-18;
 Matches 101; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 CTGCTTTTATCTAAGTTGGCATTATAAAAAGCATTGCTTATCAATTGTTGCAACG 60
 Db 156 CAGCTTTTATCTAAGTTGGCATTATAAAAAGCATTGCTTATCAATTGTTGCAACG 215
 QY 61 AACAGGTCACATCACTCAAGTCAAAATAAATCAATCATTTGATTTC 102
 Db 216 AACAGGTCACATCACTCAAGTCAAAATAAATCAATCATTTGATTTC 257
 RESULT 13
 ABT16636
 ID ABT16636 standard; DNA; 282 BP.
 XX
 AC ABT16636;
 XX
 DT 03-APR-2003 (first entry)
 XX
 XX Artificial plant chromosome related oligo SEQ ID No 48.
 DE
 XX Plant artificial chromosome; PAC; transgenic plant; vaccine;
 KW blood factor; herbicide; stress; agronomical; nutrient quality;
 KW bacterial artificial chromosome; BAC; yeast artificial chromosome; YAC;
 KW ds.
 XX
 OS Unidentified.
 OS WO200296923-A1.
 PN 05-DEC-2002.
 PD
 XX 30-MAY-2002; 2002WO-US017451.
 XX
 XX 30-MAY-2001; 2001US-0294687P.
 PR 04-JUN-2001; 2001US-0296329P.
 XX
 XX (CHRO-) CHROMOS MOLECULAR SYSTEMS INC.
 PA (AGRI-) AGRISOMA INC.
 XX
 XX Perez C, Fabijanski SF, Perkins E;
 XX WPI; 2003-140436/13.
 DR
 XX Producing artificial chromosome by introducing a nucleic acid into plant
 PT cell, selecting artificial chromosome that has one or more repeat regions
 PT with equivalent amounts of euchromatic and heterochromatic nucleic acids.
 XX
 XX Disclosure; Page 263-264; 269pp; English.
 PS
 XX The invention relates to a novel method for producing plant artificial
 CC chromosomes. The invention also relates to methods for targeting
 CC insertion of heterologous DNA into plant artificial chromosomes, methods
 CC for delivery of plant chromosomes to selected cells and tissues. The
 CC isolated plant artificial chromosome (PAC) is useful for producing a
 CC transgenic plant, which involves introducing the PAC into a plant cell.
 CC The PAC comprises a heterologous nucleic acid encoding a gene product
 CC such as enzymes, antisense RNA, tRNA, rDNA, structural proteins, marker
 CC proteins, ligands, receptors, ribozymes, therapeutic proteins, and

QY 1 CTGCTTTTATATAAGTTGGCATTATAAAAGCATTGCTTATCAATTGTTGCAAG 60
 Db |||||
 949 CAGCTTTTATATAAGTTGGCATTATAAAAGCATTGCTTATCAATTGTTGCAAG 1008
 QY 61 AACAGGTCACTATCAGTCAAAATAAAATCAATTATTGATTC 102
 Db |||||
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OM nucleic - nucleic search, using sw model

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Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	102	100.0	2408	2	US-08-482-279-69
3	102	100.0	2408	2	US-08-342-268-69
4	102	100.0	2408	3	US-09-015-988-69
5	102	100.0	2408	4	US-09-397-386-69
6	102	100.0	3484	4	US-09-308-090-1
7	102	100.0	3484	4	US-09-380-090A-1
8	102	100.0	3757	2	US-09-016-366A-13
9	102	100.0	3757	2	US-08-978-404B-19
10	102	100.0	5349	4	US-09-068-101-7
11	102	100.0	5611	4	US-09-068-101-10
12	100.4	98.4	201	1	US-08-021-667A-18
13	100.4	98.4	201	1	US-08-410-544-18
14	100.4	98.4	201	1	US-08-728-785A-18
15	100.4	98.4	4909	3	US-08-556-978B-78
16	100.4	98.4	6043	4	US-09-630-929-4
17	100.4	98.4	7652	1	US-07-590-988A-1
18	80.2	78.6	228	4	US-09-107-532A-667
19	62	60.8	38584	4	US-09-453-702B-50
20	41.6	40.8	9827	4	US-09-453-702B-66
21	32.2	31.6	11049	4	US-10-204-708-24
22	30.6	30.0	675	4	US-09-543-681A-3694
23	30.4	29.8	786431	4	US-09-751-389-3
24	30.2	29.6	4429	1	US-08-308-872B-3
25	30	29.4	2004	4	US-08-956-171E-269
26	29.6	29.0	4140	3	US-08-894-731-2
27	28.8	28.2	4359	2	US-08-566-398-23

C 28	28.8	28.2	4365	3	US-08-392-459-21	Sequence 21, Appl
C 29	28.8	28.2	4365	4	US-09-854-799-21	Sequence 21, Appl
C 30	28.8	28.2	4365	5	PCT-US91-08525-21	Sequence 21, Appl
C 31	28.8	28.2	4365	5	PCT-US93-04384-1	Sequence 1, Appl
C 32	28.6	28.0	4500	1	US-08-308-872B-1	Sequence 1, Appl
C 33	28.2	27.6	602	4	US-08-916-246-1	Sequence 1, Appl
C 34	28.2	27.6	654	4	US-09-134-001C-2801	Sequence 2801, Ap
C 35	28.2	27.6	580073	4	US-08-545-528D-1	Sequence 1, Appl
C 36	28	27.5	483	4	US-09-621-976-14383	Sequence 14383, A
C 37	28	27.5	611	3	US-09-385-982-357	Sequence 357, App
C 38	28	27.5	2099	1	US-08-299-849B-25	Sequence 25, Appl
C 39	28	27.5	2099	2	US-08-142-368A-25	Sequence 25, Appl
C 40	28	27.5	2099	3	US-08-967-727-25	Sequence 25, Appl
C 41	28	27.5	2099	3	US-08-037-230D-25	Sequence 25, Appl
C 42	28	27.5	2099	4	US-09-583-850-25	Sequence 25, Appl
C 43	28	27.5	2099	4	US-09-579-197-25	Sequence 25, Appl
C 44	28	27.5	2099	4	US-09-404-026-25	Sequence 25, Appl
C 45	28	27.5	2099	4	US-09-312-464-25	Sequence 25, Appl

ALIGNMENTS

RESULT 1
US-08-486-013-69
; Sequence 69, Application US/08486013
; Patent No. 5731149
; GENERAL INFORMATION:
; APPLICANT: Selsted, Michael E.
; TITLE OF INVENTION: Antibiotic Cryptidin Peptides and Methods
; TITLE OF INVENTION: Of Their Use
; NUMBER OF SEQUENCES: 70
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell and Flores
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: USA
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/486,013
; FILING DATE:
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/342,268
; FILING DATE: 18-NOV-1994
; APPLICATION NUMBER: US 07/930,649
; FILING DATE: 14-AUG-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/889,020
; FILING DATE: 26-MAY-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-UC 1206
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 69:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2408 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-486-013-69

Query Match 100.0% Score 102; DB 1; Length 2408;

Best Local Similarity 100.0%; Pred. No. 4.1e-20; Mismatches 0; Indels 0; Gaps 0;
Matches 102; Conservative 0;

QY 1 CTGCTTTTATACTAAGTTGGCATTATATAAAAGCATTGCTTATCAATTGTTGCAACG 60
Db CTGCTTTTATACTAAGTTGGCATTATATAAAAGCATTGCTTATCAATTGTTGCAACG 467
QY 61 AACAGTCTACTATCAGTCAAAATAAAATCAATTATTGATTTC 102
Db 468 AACAGTCTACTATCAGTCAAAATAAAATCAATTATTGATTTC 509

RESULT 2

US-08-482-279-69
; Sequence 69, Application US/08482279
; Patent No. 5840498
; GENERAL INFORMATION:
; APPLICANT: Selsted, Michael E.
; APPLICANT: Ouellette, Andre J.
; TITLE OF INVENTION: Antibiotic Cryptdin Peptides and Methods
; TITLE OF INVENTION: of Their Use
; NUMBER OF SEQUENCES: 70
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell and Flores
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: USA
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/482,279
; FILING DATE: 18-NOV-1994
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/342,268
; FILING DATE: 18-NOV-1994
; APPLICATION NUMBER: US 07/930,649
; FILING DATE: 14-AUG-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/889,020
; FILING DATE: 26-MAY-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-UC 1206
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 69:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2408 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-482-279-69

Query Match 100.0%; Score 102; DB 2; Length 2408;
Best Local Similarity 100.0%; Pred. No. 4.1e-20; Mismatches 0; Indels 0; Gaps 0;
Matches 102; Conservative 0;

QY 1 CTGCTTTTATACTAAGTTGGCATTATATAAAAGCATTGCTTATCAATTGTTGCAACG 60
Db CTGCTTTTATACTAAGTTGGCATTATATAAAAGCATTGCTTATCAATTGTTGCAACG 467
QY 61 AACAGTCTACTATCAGTCAAAATAAAATCAATTATTGATTTC 102
Db 468 AACAGTCTACTATCAGTCAAAATAAAATCAATTATTGATTTC 509

RESULT 3

US-08-342-268-69
; Sequence 69, Application US/08342268
; Patent No. 5844072
; GENERAL INFORMATION:
; APPLICANT: Selsted, Michael E.
; APPLICANT: Ouellette, Andre J.
; TITLE OF INVENTION: Antibiotic Cryptdin Peptides and Methods
; TITLE OF INVENTION: of Their Use
; NUMBER OF SEQUENCES: 70
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell and Flores
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: USA
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/342,268
; FILING DATE: 18-NOV-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/930,649
; FILING DATE: 14-AUG-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/889,020
; FILING DATE: 26-MAY-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-UC 1206
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 69:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2408 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-342-268-69

Query Match 100.0%; Score 102; DB 2; Length 2408;
Best Local Similarity 100.0%; Pred. No. 4.1e-20; Mismatches 0; Indels 0; Gaps 0;
Matches 102; Conservative 0;

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Db 408 CTGCTTTTATACTAAGTTGGCATTATATAAAAGCATTGCTTATCAATTGTTGCAACG 467
QY 61 AACAGTCTACTATCAGTCAAAATAAAATCAATTATTGATTTC 102
Db 468 AACAGTCTACTATCAGTCAAAATAAAATCAATTATTGATTTC 509

RESULT 4

US-09-015-968-69
; Sequence 69, Application US/09015968
; Patent No. 6057425
; GENERAL INFORMATION:
; APPLICANT: Selsted, Michael E.
; APPLICANT: Ouellette, Andre J.
; TITLE OF INVENTION: Antibiotic Cryptdin Peptides and Methods
; TITLE OF INVENTION: of Their Use
; NUMBER OF SEQUENCES: 70
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell and Flores

STREET: 4370 La Jolla Village Drive, Suite 700
CITY: San Diego
STATE: California
COUNTRY: USA
ZIP: 92122
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/015,968
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/482,279
FILING DATE: 07-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/342,268
FILING DATE: 18-NOV-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/930,649
FILING DATE: 14-AUG-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/889,020
FILING DATE: 26-MAY-1992
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-UC 3003
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
TELEFAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 69:
SEQUENCE CHARACTERISTICS:
LENGTH: 2408 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-09-015-968-69
Query Match 100.0%; Score 102; DB 3; Length 2408;
Best Local Similarity 100.0%; Pred. No. 4.1e-20;
Matches 102; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CTGCTTTTATCTAAGTTGGCATTATATAAAAGCATTGCTTATCAATTGTTGCAACG 60
Db 408 CTGCTTTTATCTAAGTTGGCATTATATAAAAGCATTGCTTATCAATTGTTGCAACG 467
QY 61 AACAGGTCATCTATCAGTCAAAATAAAATCAATTATTGATTTC 102
Db 468 AACAGGTCATCTATCAGTCAAAATAAAATCAATTATTGATTTC 509
RESULT 5
US-09-397-386-69
Sequence 69, Application US/09397386
Patent No. 6300470
GENERAL INFORMATION:
APPLICANT: Selsted, Michael E.
APPLICANT: Ouellette, Andre J.
TITLE OF INVENTION: Antibiotic Cryptidin Peptides and Methods
TITLE OF INVENTION: of Their Use
NUMBER OF SEQUENCES: 70
CORRESPONDENCE ADDRESS:
ADDRESSEE: Campbell and Flores
STREET: 4370 La Jolla Village Drive, Suite 700
CITY: San Diego
STATE: California
COUNTRY: USA
ZIP: 92122
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/397,386
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/015,968
FILING DATE:
APPLICATION NUMBER: US 08/482,279
FILING DATE: 07-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/342,268
FILING DATE: 18-NOV-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/930,649
FILING DATE: 14-AUG-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/889,020
FILING DATE: 26-MAY-1992
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-UC 3003
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
TELEFAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 69:
SEQUENCE CHARACTERISTICS:
LENGTH: 2408 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-09-397-386-69
Query Match 100.0%; Score 102; DB 4; Length 2408;
Best Local Similarity 100.0%; Pred. No. 4.1e-20;
Matches 102; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CTGCTTTTATCTAAGTTGGCATTATATAAAAGCATTGCTTATCAATTGTTGCAACG 60
Db 408 CTGCTTTTATCTAAGTTGGCATTATATAAAAGCATTGCTTATCAATTGTTGCAACG 467
QY 61 AACAGGTCATCTATCAGTCAAAATAAAATCAATTATTGATTTC 102
Db 468 AACAGGTCATCTATCAGTCAAAATAAAATCAATTATTGATTTC 509
RESULT 6
US-09-308-090-1
Sequence 1, Application US/09308090
Patent No. 6395963
GENERAL INFORMATION:
APPLICANT: Ohl, Stephan
APPLICANT: Van der Lee, Frederique
APPLICANT: Goddijn, Oscar
APPLICANT: Klap, Joke
APPLICANT: Sijmons, Peter
TITLE OF INVENTION: Nematode-Inducible Regulatory DNA Sequences
TITLE REFERENCE: MOG 57680
CURRENT APPLICATION NUMBER: US/09/308,090
CURRENT FILING DATE: 1999-05-14
EARLIER APPLICATION NUMBER: PCT/EP97/06472
EARLIER FILING DATE: 1997-11-18
EARLIER APPLICATION NUMBER: EP 96203213.2
EARLIER FILING DATE: 1996-11-18
NUMBER OF SEQ ID NOS: 10
SOFTWARE: Patent In Ver. 2.0
SEQ ID NO 1
LENGTH: 3484
TYPE: DNA
ORGANISM: Arabidopsis thaliana

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; NAME/KEY: CDS
; LOCATION: (3482) .. (3484)
; OTHER INFORMATION: /codon_start= 3482
; SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-308-090-1

Query Match      100.0%; Score 102; DB 4; Length 3484;
Best Local Similarity 100.0%; Pred. No. 4.3e-20;
Matches 102; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTGCTTTTATCTAAGTTGGCATTATATAAAAGCATTGCTTATCAATTGTTGCAACG 60
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Db 420 CTGCTTTTATCTAAGTTGGCATTATATAAAAGCATTGCTTATCAATTGTTGCAACG 479

QY 61 AACAGTCACTATCAGTCAAAATAAAATCAATTATTGATTC 102
   |||||||
Db 480 AACAGTCACTATCAGTCAAAATAAAATCAATTATTGATTC 521

RESULT 7
US-09-380-090A-1
; Sequence 1, Application US/09380090A
; Patent No. 6555529
; GENERAL INFORMATION:
; APPLICANT: OHL, Stephan Andreas
; SIMMONS, Peter Christiaan
; KLEIN-VAN DER LEE, Frederique
; Marianne
; GODDION, Oscar
; Klap, Joke
; TITLE OF INVENTION: NEMATODE-INDUCIBLE REGULATORY DNA
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESS: Hale and Dorr LLP
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: United States
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/380,090A
; FILING DATE: 17-May-1999
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/EP97/06472
; FILING DATE: 18-NOV-1997
; APPLICATION NUMBER: EP 96203213.2
; FILING DATE: 18-NOV-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Superko, Colleen
; REGISTRATION NUMBER: 39,850
; REFERENCE/DOCKET NUMBER: SYN-010
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 526-6000
; TELEFAX: (617) 526-5000
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3484 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHEICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Arabidopsis thaliana
; STRAIN: C24
; FEATURE:
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; NAME/KEY: CDS
; LOCATION: 3481..3484
; OTHER INFORMATION: /codon_start= 3482
; SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-380-090A-1

Query Match      100.0%; Score 102; DB 4; Length 3484;
Best Local Similarity 100.0%; Pred. No. 4.3e-20;
Matches 102; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTGCTTTTATCTAAGTTGGCATTATATAAAAGCATTGCTTATCAATTGTTGCAACG 60
   |||||||
Db 420 CTGCTTTTATCTAAGTTGGCATTATATAAAAGCATTGCTTATCAATTGTTGCAACG 479

QY 61 AACAGTCACTATCAGTCAAAATAAAATCAATTATTGATTC 102
   |||||||
Db 480 AACAGTCACTATCAGTCAAAATAAAATCAATTATTGATTC 521

RESULT 8
US-09-016-366A-13
; Sequence 13, Application US/09016366A
; Patent No. 5955431
; GENERAL INFORMATION:
; APPLICANT: Stevens, Richard L.
; APPLICANT: Huang, Chifu
; TITLE OF INVENTION: MAST CELL PROTEASE PEPTIDE
; NUMBER OF SEQUENCES: 65
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Wolf, Greenfield & Sacks, P.C.
; STREET: 600 Atlantic Avenue
; CITY: Boston
; STATE: MA
; COUNTRY: U.S.A.
; ZIP: 02210-2211
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/016,366A
; FILING DATE: January 30, 1998
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/037,090
; FILING DATE: 05-FEB-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Plumer, Elizabeth R.
; REGISTRATION NUMBER: 36,637
; REFERENCE/DOCKET NUMBER: B0801/7093
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-720-3500
; TELEFAX: 617-720-2441
; TELEX:
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3757 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; US-09-016-366A-13

Query Match      100.0%; Score 102; DB 2; Length 3757;
Best Local Similarity 100.0%; Pred. No. 4.3e-20;
Matches 102; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTGCTTTTATCTAAGTTGGCATTATATAAAAGCATTGCTTATCAATTGTTGCAACG 60
   |||||||
Db 374 CTGCTTTTATCTAAGTTGGCATTATATAAAAGCATTGCTTATCAATTGTTGCAACG 433
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QY 61 AACAGGTCACATCAGTCACAAATAAATCATTTTGGATTTC 102
 Db 434 AACAGGTCACATCAGTCACAAATAAATCATTTTGGATTTC 475

RESULT 9

US-08-978-404B-19
 ; Sequence 19, Application US/08978404B
 ; Patent No. 5968782
 ; GENERAL INFORMATION:
 ; APPLICANT: Stevens, Richard L.
 ; TITLE OF INVENTION: NAST CELL PROTEASE THAT CLEAVES
 ; TITLE OF INVENTION: FIBRINOGEN
 ; NUMBER OF SEQUENCES: 74
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSES: Wolf, Greenfield & Sacks, P.C.
 ; STREET: 600 Atlantic Avenue
 ; CITY: Boston
 ; STATE: MA
 ; COUNTRY: U.S.A.
 ; ZIP: 02210-2211
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Diskette
 ; COMPUTER: IBM Compatible
 ; OPERATING SYSTEM: DOS
 ; SOFTWARE: FastSeq for Windows Version 2.0
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/978,404B
 ; FILING DATE: 25-NOV-97
 ; CLASSIFICATION: 435
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 60/032,354
 ; FILING DATE: 04-DEC-1996
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Plumer, Elizabeth R.
 ; REGISTRATION NUMBER: 36,637
 ; REFERENCE/DOCKET NUMBER: B0801/7090
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 617-720-3500
 ; TELEFAX: 617-720-2441
 ; TELEX:
 ; INFORMATION FOR SEQ ID NO: 19:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 3757 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; US-08-978-404B-19

Query Match 100.0%; Score 102; DB 2; Length 3757;
 Best Local Similarity 100.0%; Pred. No. 4.3e-20;
 Matches 102; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTGCTTTTATCTAAGTTGGCATTATAAAAAGCATTGCTTATCAATTTGTTGCAACG 60
 Db 374 CTGCTTTTATCTAAGTTGGCATTATAAAAAGCATTGCTTATCAATTTGTTGCAACG 433

QY 61 AACAGGTCACATCAGTCACAAATAAATCATTTTGGATTTC 102
 Db 434 AACAGGTCACATCAGTCACAAATAAATCATTTTGGATTTC 475

RESULT 10

US-09-068-101-7/c
 ; Sequence 7, Application US/09068101
 ; Patent No. 6372960
 ; GENERAL INFORMATION:
 ; APPLICANT: PLANT GENETIC SYSTEMS N.V.
 ; TITLE OF INVENTION: Improved Barstar Gene
 ; FILE REFERENCE: 2121-139P
 ; CURRENT APPLICATION NUMBER: US/09/068,101
 ; CURRENT FILING DATE: 1998-08-26
 ; EARLIER APPLICATION NUMBER: EP 96202446.9

; EARLIER FILING DATE: 1996-09-03
 ; NUMBER OF SEQ ID NOS: 10
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 7
 ; LENGTH: 5349
 ; TYPE: DNA
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Description of Artificial Sequence: other nucleic
 ; OTHER INFORMATION: acid, "T-DNA of pTTS243"
 ; NAME/KEY: misc feature
 ; LOCATION: Complement(11)..(25))
 ; OTHER INFORMATION: label = RB, "T-DNA right border"
 ; FEATURE:
 ; NAME/KEY: misc feature
 ; LOCATION: Complement(98)..(331))
 ; OTHER INFORMATION: label = 3'g7, "region containing 3' untranslated
 ; OTHER INFORMATION: end of Agrobacterium T-DNA gene 7"
 ; FEATURE:
 ; NAME/KEY: misc feature
 ; LOCATION: Complement(332)..(883))
 ; OTHER INFORMATION: label = bar, "region coding for phosphinethricin
 ; OTHER INFORMATION: acetyl transferase"
 ; FEATURE:
 ; NAME/KEY: misc feature
 ; LOCATION: Complement(884)..(2258))
 ; OTHER INFORMATION: label = P35S, "35S promoter of Cauliflower Mosaic
 ; OTHER INFORMATION: Virus"
 ; FEATURE:
 ; NAME/KEY: misc feature
 ; LOCATION: (2281)..(3969)
 ; OTHER INFORMATION: label = PEI, "promoter of EI gene of rice (WO
 ; OTHER INFORMATION: 92/13956)"
 ; FEATURE:
 ; NAME/KEY: misc feature
 ; LOCATION: (3970)..(4245)
 ; OTHER INFORMATION: label = synb*, "improved barstar DNA"
 ; FEATURE:
 ; NAME/KEY: misc feature
 ; LOCATION: (4246)..(4577)
 ; OTHER INFORMATION: label = 3'chs, "region containing 3' untranslated
 ; OTHER INFORMATION: end of chalcone synthase gene"
 ; FEATURE:
 ; NAME/KEY: misc feature
 ; LOCATION: Complement(5325)..(5349))
 ; OTHER INFORMATION: label = LB, "T-DNA left border"
 ; US-09-068-101-7

Query Match 100.0%; Score 102; DB 4; Length 5349;
 Best Local Similarity 100.0%; Pred. No. 4.6e-20;
 Matches 102; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 61 AACAGGTCACATCAGTCACAAATAAATCATTTTGGATTTC 102
 Db 4825 AACAGGTCACATCAGTCACAAATAAATCATTTTGGATTTC 4784

RESULT 11

US-09-068-101-10/c
 ; Sequence 10, Application US/09068101
 ; Patent No. 6372960
 ; GENERAL INFORMATION:
 ; APPLICANT: PLANT GENETIC SYSTEMS N.V.
 ; TITLE OF INVENTION: Improved Barstar Gene
 ; FILE REFERENCE: 2121-139P
 ; CURRENT APPLICATION NUMBER: US/09/068,101
 ; CURRENT FILING DATE: 1998-08-26
 ; EARLIER APPLICATION NUMBER: EP 96202446.9

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; EARLIER FILING DATE: 1996-09-03
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn ver. 2.0
; SEQ ID NO 10
; LENGTH: 5611
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: other nucleic
; OTHER INFORMATION: acid, "plasmid pLH48"
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: Complement((39)..(317))
; OTHER INFORMATION: label = 3'nos, "region containing 3' untranslated
; OTHER INFORMATION: end of nopaline synthase gene of Agrobacterium
; OTHER INFORMATION: T-DNA"
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: Complement((318)..(869))
; OTHER INFORMATION: label = bar, "region coding for phosphinothricin
; OTHER INFORMATION: acetyl transferase"
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: Complement((870)..(1702))
; OTHER INFORMATION: label = P35S, "35S promoter of Cauliflower Mosaic
; OTHER INFORMATION: Virus"
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1740)..(2284)
; OTHER INFORMATION: label = PTA29, "promoter of TA29 gene of Nicotiana
; OTHER INFORMATION: tabacum"
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (2285)..(2560)
; OTHER INFORMATION: label = synb*, "improved barstar DNA"
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (2561)..(2892)
; OTHER INFORMATION: label = 3'chs, "region containing 3' untranslated
; OTHER INFORMATION: end of chalcone synthase gene"
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US-09-068-101-10

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Query Match      100.0%; Score 102; DB 4; Length 5611;
Best Local Similarity 100.0%; Pred. No. 4.6e-20;
Matches 102; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 61 AACAGGTCATCATCAGTCAAAATAAAATCAATTATTGATTC 102
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RESULT 12
US-08-021-667A-18
; Sequence 18, Application US/08021667A
; Patent No. 5434049
; GENERAL INFORMATION:
; APPLICANT: Okano, Kazunori
; APPLICANT: Kambara, Hideki
; TITLE OF INVENTION: POLYNUCLEOTIDE CAPTURING TIP AND
; TITLE OF INVENTION: POLYNUCLEOTIDE PREPARATIVE METHOD AND DETECTION
; TITLE OF INVENTION: METHOD USING SAME
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Antonelli, Terry, Stout & Kraus
; STREET: Suite 600, 1919 Pennsylvania Ave., NW
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20006

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; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/021,667A
; FILING DATE: 19930224
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Terry, David T.
; REGISTRATION NUMBER: 20,178
; REFERENCE/DOCKET NUMBER: 520.31930X00
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-828-0300
; TELEFAX: 202-828-0380
; TELEX: 440280/248545
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 201 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: YES
; ANTI-SENSE: NO
;
US-08-021-667A-18
Query Match      98.4%; Score 100.4; DB 1; Length 201;
Best Local Similarity 99.0%; Pred. No. 8.1e-20;
Matches 101; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CTGCTTTTATACAAAGTTGGCATTATAAAAGCAATGCTTATCAATTGTTGCAACG 60
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Db 43 CAGCTTTTATACAAAGTTGGCATTATAAAAGCAATGCTTATCAATTGTTGCAACG 102
    |||||||

QY 61 AACAGGTCATCATCAGTCAAAATAAAATCAATTATTGATTC 102
    |||||||
Db 103 AACAGGTCATCATCAGTCAAAATAAAATCAATTATTGATTC 144
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RESULT 13
US-08-410-544-18
; Sequence 18, Application US/08410544
; Patent No. 5607646
; GENERAL INFORMATION:
; APPLICANT: Okano, Kazunori
; APPLICANT: Kambara, Hideki
; TITLE OF INVENTION: POLYNUCLEOTIDE CAPTURING TIP AND
; TITLE OF INVENTION: POLYNUCLEOTIDE PREPARATIVE METHOD AND DETECTION
; TITLE OF INVENTION: METHOD USING SAME
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Antonelli, Terry, Stout & Kraus
; STREET: Suite 600, 1919 Pennsylvania Ave., NW
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20006
;
COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/410,544
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/021,667
; FILING DATE: 24-FEB-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Terry, David T.

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Fri Sep 10 09:49:25 2004

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2315 AACAGTCACTATCAGTCAAAATAAAATCATTATTGATTTC 2274

Search completed: September 9, 2004, 21:21:19
Job time : 23.4903 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: September 9, 2004, 13:30:05 ; Search time 184.482 Seconds
(without alignments)
3730.479 Million cell updates/sec

Title: US-10-082-772B-4
Perfect score: 162
Sequence: 1 tctgttacaggtcactaataa.....agctttttataactaacttg 162

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 3373863 seqs, 2124099041 residues
Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_29Jan04:*

- 1: Geneseqn1980s:*
- 2: Geneseqn1990s:*
- 3: Geneseqn2000s:*
- 4: Geneseqn2001as:*
- 5: Geneseqn2001bs:*
- 6: Geneseqn2002as:*
- 7: Geneseqn2003as:*
- 8: Geneseqn2003bs:*
- 9: Geneseqn2003cs:*
- 10: Geneseqn2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	162	100.0	162	4	AAF61420 E. coli a
2	160.4	99.0	243	4	AAF61418 Bacteriop
3	160.4	99.0	248	8	ACC85316 Recombina
4	160.4	99.0	282	7	ACC44676 Murine rD
5	160.4	99.0	282	7	ABT16636 Artificia
6	160.4	99.0	610	5	AAF79770 Bacteriop
7	160.4	99.0	1469	7	ABQ80306 Lambda fr
8	160.4	99.0	1469	7	ACC83020 Bacteriop
9	160.4	99.0	1763	2	AAC30709 Rat neuro
10	160.4	99.0	4346	7	ABT16615 Plasmid p
11	160.4	99.0	4346	7	ABT16615 Artificia
12	160.4	99.0	4909	2	AAT18924 Plasmid p
13	160.4	99.0	5641	4	AAF30800 Vector pl
14	160.4	99.0	5670	4	AAF30801 Vector pl
15	160.4	99.0	5826	4	AAF30798 Vector pl
16	160.4	99.0	6071	4	AAF30799 Vector pl
17	160.4	99.0	7652	2	AAQ45682 Sequencin
18	158.8	98.0	243	4	AAF61421 E. coli a
19	152.4	94.1	17458	6	ABQ82142 Acceptor
20	152.4	94.1	17458	6	ABQ82142 Acceptor
21	152.4	94.1	17476	6	ABQ82141 Acceptor
22	152.4	94.1	17476	6	ABQ82141 Acceptor
23	152.4	94.1	17681	6	ABQ82143 Acceptor

C	24	152.4	94.1	17681	6	ABQ82143	Abq82143	Acceptor
C	25	150.8	93.1	4204	3	AAC55522	Aac55522	Donor pla
C	26	150.8	93.1	4208	3	AAC55523	Aac55523	Donor pla
C	27	150.8	93.1	4470	3	AAC55521	Aac55521	Donor pla
C	28	150.8	93.1	4470	7	ABZ58767	Abz58767	Destinati
C	29	150.8	93.1	4892	8	ADA50329	Ada50329	Plasmid v
C	30	150.8	93.1	4939	3	AAC55525	Aac55525	Donor pla
C	31	150.8	93.1	5584	3	AAC55632	Aac55632	Donor pla
C	32	150.8	93.1	5584	7	ABZ58766	Abz58766	Donor pla
C	33	150.8	93.1	18691	6	ABQ82130	Abq82130	Acceptor
C	34	150.8	93.1	18691	6	ABQ82130	Abq82130	Acceptor
C	35	150.6	93.0	233	3	AAC55382	Aac55382	Recombina
C	36	150.6	93.0	233	7	ACC59568	Acc59568	Nucleic a
C	37	149.2	92.1	4165	3	AAC55524	Aac55524	Donor pla
C	38	149.2	92.1	4204	3	AAC55522	Aac55522	Donor pla
C	39	149.2	92.1	4208	3	AAC55523	Aac55523	Donor pla
C	40	149.2	92.1	4428	7	ABZ58768	Abz58768	Destinati
C	41	149.2	92.1	4470	3	AAC55521	Aac55521	Donor pla
C	42	149.2	92.1	4470	7	ABZ58767	Abz58767	Destinati
C	43	149.2	92.1	4627	7	ABZ58769	Abz58769	Destinati
C	44	149.2	92.1	4627	7	ABZ58770	Abz58770	Destinati
C	45	149.2	92.1	4892	8	ADA50329	Ada50329	Plasmid v

ALIGNMENTS

RESULT 1
AAF61420
ID AAF61420 standard; DNA; 162 BP.
XX
AC AAF61420;
XX
DT 05-JUN-2001 (first entry)
XX
DE E. coli attr DNA fragment.
XX
KW Sequence-specific recombination; SSR; integrase; gene therapy; somatic;
KW targeted integration; attr; ds.
XX
OS Escherichia coli.
XX
PN DE19941186-A1.
XX
PD 01-MAR-2001.
XX
PF 30-AUG-1999; 99DE-01041186.
XX
PR 30-AUG-1999; 99DE-01041186.
XX
PA (DROE/) DROEGE P.
XX
PI Droege P;
XX
DR WPI; 2001-246016/26.
XX
PT Sequence-specific recombination of DNA in eukaryotes, useful particularly
PT for somatic cell gene therapy, uses an integrase to effect recombination
PT between att sites.
XX
PS Claim 3; Page 14; 24pp; German.
XX
CC This invention describes a novel sequence-specific recombination (SSR) of
CC DNA in a eukaryotic cell, comprising introducing two DNA sequences (I,
CC II) into a cell, using an integrase (Int) to effect SSR. The invention
CC also describes (i) a nucleic acid comprising a 243 base pair sequence
CC (III), fully defined in the specification, or its derivatives; and (2)
CC (III), containing (III), or its derivatives, plus a therapeutic gene, or
CC its derivatives. The method is particularly used in somatic gene therapy
CC in humans and animals, but can be applied more generally for gene
CC transfer to animal or plant cells. The method is simple and controllable,
CC and provides stable and targeted integration of selected DNA sequences

SQ Sequence 162 BP; 43 A; 22 C; 22 G; 75 T; 0 U; 0 Other;

Query Match 100.0%; Score 162; DB 4; Length 162;
 Best Local Similarity 100.0%; Pred. No. 4.3e-25;
 Matches 162; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCTGTTACAGGTCACTAATACCATCTAAGTAGTTGATTCTAGTGAAGTGCATATGTTGTG 60
 |||||
 DB 1 TCTGTTACAGGTCACTAATACCATCTAAGTAGTTGATTCTAGTGAAGTGCATATGTTGTG 60
 |||||

QY 61 TTTTACAGTATTATGAGTCTGTTTTTATGCAAAATCTAATTAATATATGATATTTA 120
 |||||
 DB 61 TTTTACAGTATTATGAGTCTGTTTTTATGCAAAATCTAATTAATATATGATATTTA 120
 |||||

QY 121 TATCATTTACGTTCTCGTTCAGCTTTTATATACTAACTTG 162
 |||||
 DB 121 TATCATTTACGTTCTCGTTCAGCTTTTATATACTAACTTG 162
 |||||

RESULT 2
 AAF61418
 ID AAF61418 standard; DNA; 243 BP.
 XX
 AC AAF61418;
 XX
 DT 05-JUN-2001 (first entry)
 XX
 DE Bacteriophage lambda attP DNA fragment.
 XX
 KW Sequence-specific recombination; SSR; integrase; gene therapy; somatic;
 XX targeted integration; attP; ds.
 XX
 OS Bacteriophage lambda.
 XX
 PN DE19941186-A1.
 XX
 PD 01-MAR-2001.
 XX
 PF 30-AUG-1999; 99DE-01041186.
 XX
 PR 30-AUG-1999; 99DE-01041186.
 XX
 PA (DROE/) DROEGE P.
 XX
 PI Droegge P;
 XX
 DR WPI; 2001-246016/26.
 XX
 PT Sequence-specific recombination of DNA in eukaryotes, useful particularly
 XX for somatic cell gene therapy, uses an integrase to effect recombination
 XX between att sites.
 XX
 PS Claim 2; Page 13; 24pp; German.
 XX
 CC This invention describes a novel sequence-specific recombination (SSR) of
 CC DNA in a eukaryotic cell, comprising introducing two DNA sequences (I,
 CC II) into a cell, using an integrase (Int) to effect SSR. The invention
 CC also describes (1) a nucleic acid comprising a 243 base pair sequence
 CC (III), fully defined in the specification, or its derivatives; and (2)
 CC vector containing (III), or its derivatives, plus a therapeutic gene, or
 CC its derivatives. The method is particularly used in somatic gene therapy
 CC in humans and animals, but can be applied more generally for gene
 CC transfer to animal or plant cells. The method is simple and controllable,
 CC and provides stable and targeted integration of selected DNA sequences
 CC

SQ Sequence 243 BP; 74 A; 34 C; 33 G; 102 T; 0 U; 0 Other;

Query Match 99.0%; Score 160.4; DB 4; Length 243;
 Best Local Similarity 99.4%; Pred. No. 9.3e-25;
 Matches 161; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TCTGTTACAGGTCACTAATACCATCTAAGTAGTTGATTCTAGTGAAGTGCATATGTTGTG 60
 |||||
 DB 1 TCTGTTACAGGTCACTAATACCATCTAAGTAGTTGATTCTAGTGAAGTGCATATGTTGTG 60
 |||||

Db 1 TCTGTTACAGGTCACTAATACCATCTAAGTAGTTGATTCTAGTGAAGTGCATATGTTGTG 60
 QY 61 TTTTACAGTATTATGAGTCTGTTTTTATGCAAAATCTAATTAATATATGATATTTA 120
 |||||
 Db 61 TTTTACAGTATTATGAGTCTGTTTTTATGCAAAATCTAATTAATATATGATATTTA 120
 |||||

QY 121 TATCATTTACGTTCTCGTTCAGCTTTTATATACTAACTTG 162
 |||||
 Db 121 TATCATTTACGTTCTCGTTCAGCTTTTATATACTAACTTG 162
 |||||

RESULT 3
 ACC85316
 ID ACC85316 standard; DNA; 248 BP.
 XX
 AC ACC85316;
 XX
 DT 18-SEP-2003 (first entry)
 XX
 DE Recombinase lambda integrase attP DNA recognition sequence.
 XX
 KW Vegetable plastid transformation; transgenic; recognition sequence;
 XX plant; site-specific integration; nutrition; seed production;
 XX chemical production; ds.
 XX
 OS Unidentified.
 XX
 PN WO2003054201-A1.
 XX
 PD 03-JUL-2003.
 XX
 PF 16-DEC-2002; 2002WO-EP014303.
 XX
 PR 20-DEC-2001; 2001DE-01063159.
 XX
 PA (SUNG-) SUNGENE GMBH & CO KGAA.
 XX
 PI Biesgen C;
 XX
 DR WPI; 2003-541820/51.
 XX
 PT Site-specific integration of DNA into plastid DNA, useful for making
 XX transgenic plants used e.g. as food, by recombinase-mediated insertion.
 XX
 PS Disclosure; Page 35; 164pp; German.
 XX
 CC The present invention relates to a method for the site-specific
 CC integration of a DNA sequence into the plastid DNA of a plant or its
 CC derived cells. Transgenic plants in which a DNA sequence has been
 CC integrated, also their cell cultures, organs, tissues etc. are useful in
 CC human or animal nutrition, to produce seeds, and to produce
 CC pharmaceuticals or fine chemicals, e.g. enzymes, vitamins, amino acids,
 CC flavourings and aromatizing agents, dyes, antibodies and vaccines. The
 CC present sequence is a recognition sequence shown in the exemplification
 CC of the invention
 XX

SQ Sequence 248 BP; 76 A; 35 C; 34 G; 103 T; 0 U; 0 Other;

Query Match 99.0%; Score 160.4; DB 8; Length 248;
 Best Local Similarity 99.4%; Pred. No. 9.3e-25;
 Matches 161; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TCTGTTACAGGTCACTAATACCATCTAAGTAGTTGATTCTAGTGAAGTGCATATGTTGTG 60
 |||||
 Db 6 TCTGTTACAGGTCACTAATACCATCTAAGTAGTTGATTCTAGTGAAGTGCATATGTTGTG 65
 |||||

QY 61 TTTTACAGTATTATGAGTCTGTTTTTATGCAAAATCTAATTAATATATGATATTTA 120
 |||||
 Db 66 TTTTACAGTATTATGAGTCTGTTTTTATGCAAAATCTAATTAATATATGATATTTA 125
 |||||

QY 121 TATCATTTACGTTCTCGTTCAGCTTTTATATACTAACTTG 162
 |||||
 Db 126 TATCATTTACGTTCTCGTTCAGCTTTTATATACTAACTTG 167
 |||||

RESULT 4
ACCA4676
ID ACCA4676 standard; DNA; 282 BP.
XX
XX ACCA4676;
XX
XX
XX 29-MAY-2003 (first entry)
XX
XX Murine rDNA PCR primer SEQ ID NO:72.
XX
XX Chromosome-based platform: artificial chromosome; eukaryotic chromosome;
XX att site; integrase; recombinase; Aces; gene therapy; transgenic animal;
XX platform artificial chromosome expression system; gene; ds.
XX
XX Mus musculus.
XX OS Synthetic.
XX
XX
XX WO200297059-A2.
XX
XX
XX 05-DEC-2002.
XX
XX 30-MAY-2002; 2002WO-US017452.
XX
XX 30-MAY-2001; 2001US-0294758P.
XX 21-MAR-2002; 2002US-0366891P.
XX
XX (CHRO-) CHROMOS MOLECULAR SYSTEMS INC.
XX Perkins E, Perez C, Lindenbaum M, Greene A, Leung J, Fleming E;
XX Stewart S, Shellard J;
XX WPI; 2003-140461/13.
XX
XX Novel eukaryotic chromosome comprising one or many att sites which
XX permits site-directed integration in the presence of lambda-integrase,
XX useful for site-specific recombination-directed integration of DNA of
XX interest.
XX
XX Example 2; Page 207; 272pp; English.
XX
XX The present invention describes a eukaryotic chromosome (I) comprising
XX one or several att sites, where an att site is heterologous to the
XX chromosome, and permits site-directed integration in the presence of
XX lambda-integrase. Also described: (i) a platform artificial chromosome
XX expression system (Aces) (ii) comprising several sites that participate
XX in recombinase catalysed recombination; and (2) a method (M1) for
XX introducing a heterologous nucleic acid into a platform artificial
XX chromosome. (I) can be used in gene therapy. (M1) is useful for
XX introducing a heterologous nucleic acid molecule into a platform
XX artificial chromosome, preferably an Aces. (ii) is useful for producing a
XX transgenic animal (e.g. a fish, insect, reptile, amphibian, arachnid, or
XX mammal) by introducing (ii) by cell fusion, lipid-mediated transfection,
XX by a carrier system, microinjection, microcell fusion, electroporation,
XX microprojectile bombardment or direct DNA transfer into an embryonic
XX cell, preferably a stem cell or an embryo. (ii) comprises a heterologous
XX nucleic acid that encodes a therapeutic product which is useful for
XX making a library of Aces comprising random portions of a genome. ACCA4612
XX to ACCA4732 and ABP96650 to ABP96657 represent sequences used in the
XX exemplification of the present invention
XX
XX Sequence 282 BP; 79 A; 49 C; 39 G; 115 T; 0 U; 0 Other;
XX
XX Query Match 99.0%; Score 160.4; DB 7; Length 282;
XX Best Local Similarity 99.4%; Pred. No. 9.3e-25;
XX Matches 161; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
XX 1 TCTGTTACAGTCTACTAATACCATCTAGTAGTTGATTCATGATGATGATGTTG 60
XX
XX 15 TCTGTTACAGTCTACTAATACCATCTAGTAGTTGATTCATGATGATGATGTTG 74
XX
XX 61 TTTTACAGTATTAGTAGTCTGTTTTTATGCAAAATCTAATTAATATGATATTA 120

Db 75 TTTTACAGTATTAGTAGTCTGTTTTTATGCAAAATCTAATTAATATGATATTA 134
Qy 121 TATCAATTTACGTTTCCTCGTTTCAGCTTTTTTATATACTAACTTG 162
Db 135 TATCAATTTACGTTTCCTCGTTTCAGCTTTTTTATATACTAACTTG 176
RESULT 5
ABTI1636
ID ABTI1636 standard; DNA; 282 BP.
XX
XX ABTI1636;
XX
XX 03-APR-2003 (first entry)
XX
XX Artificial plant chromosome related oligo SEQ ID No 48.
XX
XX Plant artificial chromosome; PAC; transgenic plant; vaccine;
XX blood factor; herbicide; stress; agronomical; nutrient quality;
XX bacterial artificial chromosome; BAC; yeast artificial chromosome; YAC;
XX ds.
XX
XX Unidentified.
XX
XX WO200296923-A1.
XX
XX 05-DEC-2002.
XX
XX 30-MAY-2002; 2002WO-US017451.
XX
XX 30-MAY-2001; 2001US-0294687P.
XX 04-JUN-2001; 2001US-0296329P.
XX
XX (CHRO-) CHROMOS MOLECULAR SYSTEMS INC.
XX (AGRI-) AGRISOMA INC.
XX Perez C, Fabijanski SF, Perkins E;
XX
XX WPI; 2003-140436/13.
XX
XX Producing artificial chromosome by introducing a nucleic acid into plant
XX cell, selecting artificial chromosome that has one or more repeat regions
XX with equivalent amounts of euchromatic and heterochromatic nucleic acids.
XX
XX Disclosure; Page 263-264; 269pp; English.
XX
XX The invention relates to a novel method for producing plant artificial
XX chromosomes. The invention also relates to methods for targeting
XX insertion of heterologous DNA into plant artificial chromosomes, methods
XX for delivery of plant chromosomes to selected cells and tissues. The
XX isolated plant artificial chromosome (PAC) is useful for producing a
XX transgenic plant, which involves introducing the PAC into a plant cell.
XX The PAC comprises a heterologous nucleic acid encoding a gene product
XX such as enzymes, antisense RNA, rRNA, tRNA, structural proteins, marker
XX proteins, ligands, receptors, ribozymes, therapeutic proteins, and
XX biopharmaceutical proteins, vaccines, blood factors, antigens, hormones,
XX cytokines, growth factors, antibodies, or a product that provides for
XX resistance to diseases, insects, herbicides, or stress in a plant. The
XX heterologous nucleic acid optionally encodes a product that provides an
XX agronomically important trait in the plant, e.g. a product that alters
XX nutrient use and/or improves the nutrient quality of the plant. The
XX heterologous nucleic acid is contained within a bacterial artificial
XX chromosome (BAC) or a yeast artificial chromosome (YAC). This
XX polynucleotide sequence represents an oligo relating to the method for
XX producing plant artificial chromosomes of the invention
XX
XX Sequence 282 BP; 79 A; 49 C; 39 G; 115 T; 0 U; 0 Other;
XX
XX Query Match 99.0%; Score 160.4; DB 7; Length 282;
XX Best Local Similarity 99.4%; Pred. No. 9.3e-25;
XX Matches 161; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TCTGTTACAGGTCACCTAATACCATCTAAGTAGTTCATGATGACTGCATATGTTGTG 60
 Db 15 TCTGTTACAGGTCACCTAATACCATCTAAGTAGTTCATGATGACTGCATATGTTGTG 74
 QY 61 TTTTACAGTATTATGCTAGTCTGCTTTTATGCAAAATCTAATTTAATATATTGATATTTA 120
 Db 75 TTTTACAGTATTATGCTAGTCTGCTTTTATGCAAAATCTAATTTAATATATTGATATTTA 134
 QY 121 TATCATTTTACGTTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 162
 Db 135 TATCATTTTACGTTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 176
 RESULT 6
 AAF79770
 ID AAF79770 standard; DNA; 610 BP.
 AC AAF79770;
 XX
 DT 29-MAY-2001 (first entry)
 DE Bacteriophage lambda attachment P region.
 KW Attachment P region; attP; recombination; marker gene removal; ds.
 OS Bacteriophage lambda.
 XX WO200121780-A2.
 PN 29-MAR-2001.
 PD
 XX 15-SEP-2000; 2000WO-GB003543.
 PF 17-SEP-1999; 99GB-00021937.
 XX (UYLE-) UNIV LEEDS.
 PA Meyer P, Zubko E;
 PI WPI; 2001-266072/27.
 XX Removing a part of a transgene which has been integrated into a genome
 PT comprises inducing intrachromosomal homologous recombination between the
 PT attachment P regions of bacteriophage lambda flanking the transgene.
 XX Claim 8; Fig 3D; 25pp; English.
 PS The present invention describes a method of removing a transgene marker
 CC by flanking the transgene with a bacteriophage lambda attachment P (attP)
 CC region and inducing homologous recombination between attP regions so that
 CC the transgene is removed. This is useful in the production of transgenic
 CC plants with less risk of inter-species transmission of marker genes,
 CC which often encode proteins associated with, for example, herbicide and
 CC antibiotic resistance. The present sequence is the attP coding region
 XX
 SQ Sequence 610 BP; 164 A; 108 C; 110 G; 228 T; 0 U; 0 Other;
 Query Match 99.0%; Score 160.4; DB 5; Length 610;
 Best Local Similarity 99.4%; Pred. No. 9.3e-25;
 Matches 161; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 TCTGTTACAGGTCACCTAATACCATCTAAGTAGTTCATGATGACTGCATATGTTGTG 60
 Db 139 TCTGTTACAGGTCACCTAATACCATCTAAGTAGTTCATGATGACTGCATATGTTGTG 198
 QY 61 TTTTACAGTATTATGCTAGTCTGCTTTTATGCAAAATCTAATTTAATATATTGATATTTA 120
 Db 199 TTTTACAGTATTATGCTAGTCTGCTTTTATGCAAAATCTAATTTAATATATTGATATTTA 258
 QY 121 TATCATTTTACGTTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 162
 Db 259 TATCATTTTACGTTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 300

RESULT 7
 ABQ80306
 ID ABQ80306 standard; DNA; 1469 BP.
 AC ABQ80306;
 XX
 DT 27-JUN-2003 (first entry)
 DE Lambda fragment in plasmid DNA.
 XX
 KW Primer; PCR; amplify; lambda phage; printer material; insertion; SNP;
 KW deletion; single nucleotide polymorphism; sequencing; diagnosis; ss.
 XX
 OS Synthetic.
 XX WO2003027991-A1.
 PN 03-APR-2003.
 PD
 XX 24-SEP-2002; 2002WO-JP009766.
 PF 25-SEP-2001; 2001JP-00291249.
 XX (DNAF-) DNAFORM KK.
 PA (RIKE) RIKEN KK.
 XX Hayashizaki Y;
 PI WPI; 2003-354676/33.
 DR
 XX Printed material useful as a delivery and storage system for oligomer
 PT and/or polymer, comprises a support having an oligomer and/or polymer
 PT applied on it.
 XX
 PS Example 1; Page 31-32; 91pp; English.
 XX The sequences given in ABQ80304-05 are primers which were used to amplify
 CC DNA for use in the material of the invention. The primers amplify a 1377
 CC bp portion of lambda phage DNA contained in a plasmid. The amplified
 CC sequence (ABQ80306) was attached to the printer material of the invention
 CC which comprises at least one support having at least one oligomer and/or
 CC polymer applied on it. The printed material is useful in a method for
 CC synthesising DNA where the product of amplification and/or ligation is
 CC cDNA and/or full-length cDNA which is recovered and used for
 CC determination of nucleotide insertion/deletion, single nucleotide
 CC polymorphism (SNP) and sequencing analysis, in a diagnostic method for
 CC determination of nucleotide insertion/deletion, or SNP analysis.
 CC Optionally, the cDNA and/or full-length cDNA is useful for the peptide,
 CC polypeptide or protein expression. The printed material is useful in
 CC research applications, or for providing scientists with oligomer and/or
 CC polymers from the printed materials easily and immediately. From the
 CC printed material, at least an oligomer and/or polymer can be obtained
 CC immediately and directly, without need to make a request for it. The
 CC oligomers and/or polymers can be delivered and stored easily with reduced
 CC labour and time while eliminating the need to use special equipment or
 CC facilities. Thus, the printed material is a quick, efficient and
 CC inexpensive sample delivery system
 XX
 SQ Sequence 1469 BP; 411 A; 300 C; 280 G; 478 T; 0 U; 0 Other;
 Query Match 99.0%; Score 160.4; DB 7; Length 1469;
 Best Local Similarity 99.4%; Pred. No. 9.2e-25;
 Matches 161; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 TCTGTTACAGGTCACCTAATACCATCTAAGTAGTTCATGATGACTGCATATGTTGTG 60
 Db 808 TCTGTTACAGGTCACCTAATACCATCTAAGTAGTTCATGATGACTGCATATGTTGTG 867
 QY 61 TTTTACAGTATTATGCTAGTCTGCTTTTATGCAAAATCTAATTTAATATATTGATATTTA 120
 Db 868 TTTTACAGTATTATGCTAGTCTGCTTTTATGCAAAATCTAATTTAATATATTGATATTTA 927

QY 121 TATCATTTTACGTTTCTCGTTACGTTTATTAATACTG 162
 DE |||||||
 Db 928 TATCATTTTACGTTTCTCGTTACGTTTATTAATACTG 969

RESULT 8
 ACC83020
 ID ACC83020 standard; DNA; 1469 BP.
 XX
 AC ACC83020;
 XX
 DT 27-AUG-2003 (first entry)
 DE Bacteriophage lambda DNA, SEQ ID NO:3 used in the invention.
 XX
 KW Oligomer storage; oligomer delivery; ds.
 OS Bacteriophage lambda.
 XX
 PN WO2003040360-A1.
 XX
 PD 15-MAY-2003.
 XX
 PF 05-NOV-2002; 2002WO-JP011492.
 XX
 PR 05-NOV-2001; 2001JP-00339217.
 XX
 PA (RIKE) RIKEN KK.
 PA (DNAF-) DNAFORM KK.
 PA (HAYA/) HAYASHIZAKI Y.
 XX
 PI Hayashizaki Y;
 XX
 DR WPI; 2003-441569/41.
 XX
 PT New support useful for storing and/or delivering an oligomer and/or
 PT polymer applied on support, has oligomer and/or polymer applied on it,
 PT and a loose-leaf sheet or a card.
 XX
 PS Example 1; Page 30-31; 70pp; English.
 CC
 CC The invention relates to a method for storing and/or delivering an
 CC oligomer and/or polymer applied on support. The support has oligomer
 CC and/or polymer applied on it, and is in the form of loose-leaf sheet or a
 CC card. The support is useful for storing and/or delivering an oligomer
 CC and/or polymer applied on it. The present sequence is Bacteriophage
 CC lambda DNA used in the exemplification of the invention
 XX
 SQ Sequence 1469 BP; 411 A; 300 C; 280 G; 478 T; 0 U; 0 Other;

Query Match 99.0%; Score 160.4; DB 7; Length 1469;
 Best Local Similarity 99.4%; Pred. No. 9.2e-25;
 Matches 161; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TCTGTTACAGTCTCAATACCATCTAAGTAGTTGATTCATAGTGCATGTTGTG 60
 Db 808 TCTGTTACAGTCTCAATACCATCTAAGTAGTTGATTCATAGTGCATGTTGTG 867

QY 61 TTTTACAGTATTATGAGTCTGTTTTTATGCAAAATCTAATTTAATATATTGATTTA 120
 Db 868 TTTTACAGTATTATGAGTCTGTTTTTATGCAAAATCTAATTTAATATATTGATTTA 927

QY 121 TATCATTTTACGTTTCTCGTTACGTTTATTAATACTG 162
 DE |||||||
 Db 928 TATCATTTTACGTTTCTCGTTACGTTTATTAATACTG 969

RESULT 9
 AAZ30709/c

ID AAZ30709 standard; cDNA; 1763 BP.

XX
 AC AAZ30709;
 XX

DT 05-JAN-2000 (first entry)
 XX
 DE Rat neuronal immediate early gene cDNA clone R280.
 XX
 KW Immediate early gene; IEG; neuron; brain; function; growth factor;
 KW transcription factor; signal transduction; cytoskeletal protein;
 KW metabolic enzyme; learning; memory; synaptic transmission; tolerance;
 KW neuronal plasticity; ds.
 XX
 OS Rattus sp.
 XX
 PN WO9940225-A1.
 XX
 PD 12-AUG-1999.
 XX
 PF 05-FEB-1999; 99WO-US002462.
 XX
 PR 09-FEB-1998; 98US-0074135P.
 PR 12-FEB-1998; 98US-0074518P.
 XX
 PA (UYJO) UNIV JOHNS HOPKINS SCHOOL MEDICINE.
 PA (BADI) BASF-LYNX BIOSCIENCE AG.
 XX
 PI Worley PF, Lanahan A, Goetz B, Hiemisch H, Kuner R, Scheek S;
 PI Nikolich K, Zhukovski E;
 XX
 DR WPI; 1999-590697/50.
 XX
 PT Novel genes and polypeptides, useful for treating conditions related to a
 PT deficiency in nIEG responsiveness to a stimulus.
 XX
 PS Claim 1; Page 114-115; 134pp; English.
 CC
 CC This sequence represents rat neuronal immediate early gene (IEG) cDNA
 CC clone R280. An IEG is a gene whose expression is rapidly increased
 CC immediately following a stimulus e.g., neuronal stimulation. Such
 CC neuronal IEGs have been found to encode a variety of proteins, including
 CC transcription factors, cytoskeletal proteins, growth factors and
 CC metabolic enzymes, as well as proteins involved in signal transduction.
 CC The identification of neuronal IEGs and the proteins they encode may
 CC provide important information about the function of neurons in, for
 CC example, learning, memory, synaptic transmission, tolerance and neuronal
 CC plasticity. Neuronal IEGs, neuronal IEG protein products, cells
 CC expressing neuronal IEGs and antibodies against neuronal IEG proteins can
 CC be used to treat an animal with a deficiency in neuronal IEG responsiveness
 CC to stimuli, such that the effect of the deficiency is minimised. The
 CC deficiency may be a reduced or elevated level of expression of an IEG.
 CC The neuronal stimulus comprises a maximal electroconvulsive seizure and
 CC its effects influence learning or memory. The IEGs and protein products
 CC are useful in identifying compounds that modulate the expression or
 CC activity of IEG nucleic acids or proteins, respectively
 XX
 SQ Sequence 1763 BP; 478 A; 402 C; 452 G; 424 T; 0 U; 7 Other;

Query Match 99.0%; Score 160.4; DB 2; Length 1763;
 Best Local Similarity 99.4%; Pred. No. 9.2e-25;
 Matches 161; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TCTGTTACAGTCTCAATACCATCTAAGTAGTTGATTCATAGTGCATGTTGTG 60
 Db 431 TCTGTTACAGTCTCAATACCATCTAAGTAGTTGATTCATAGTGCATGTTGTG 372

QY 61 TTTTACAGTATTATGAGTCTGTTTTTATGCAAAATCTAATTTAATATATTGATTTA 120
 Db 371 TTTTACAGTATTATGAGTCTGTTTTTATGCAAAATCTAATTTAATATATTGATTTA 312

QY 121 TATCATTTTACGTTTCTCGTTACGTTTATTAATACTG 162
 Db 311 TATCATTTTACGTTTCTCGTTACGTTTATTAATACTG 270

RESULT 10
 ACC44716

ID ACC44716 standard; DNA; 4346 BP.
XX ACC44716;
XX
DT 29-MAY-2003 (first entry)
XX
DE Plasmid pSV40193attPsePUR nucleotide sequence SEQ ID NO:113.
XX
KW Chromosome-based platform; artificial chromosome; eukaryotic chromosome;
XX att site; integrase; recombinase; ACes; gene therapy; transgenic animal;
KW Platform artificial chromosome expression system; gene; ds.
XX
OS Bacteriophage lambda.
XX Synthetic.
XX
XX WO200297059-A2.
XX
XX 05-DEC-2002.
XX
XX 30-MAY-2002; 2002WO-US017452.
XX
XX 30-MAY-2001; 2001US-0294758P.
XX 21-MAR-2002; 2002US-0366891P.
XX
XX (CHRO-) CHROMOS MOLECULAR SYSTEMS INC.
XX
XX Perkins E, Perez C, Lindenbaum M, Greene A, Leung J, Fleming E;
XX Stewart S, Shellard J;
XX
XX WPI; 2003-140461/13.
XX
XX Novel eukaryotic chromosome comprising one or many att sites which
XX permits site-directed integration in the presence of lambda-integrase,
XX useful for site-specific recombination-directed integration of DNA of
XX interest.
XX
XX Example 3; Page 244-245; 272pp; English.
XX
XX The present invention describes a eukaryotic chromosome (I) comprising
XX one or several att sites, where an att site is heterologous to the
XX chromosome, and permits site-directed integration in the presence of
XX lambda-integrase. Also described: (1) a platform artificial chromosome
XX expression system (ACes) (II) comprising several sites that participate
XX in recombinase catalysed recombination; and (2) a method (M1) for
XX introducing a heterologous nucleic acid into a platform artificial
XX chromosome. (I) can be used in gene therapy. (M1) is useful for
XX introducing a heterologous nucleic acid molecule into a platform
XX artificial chromosome, preferably an ACes. (II) is useful for producing a
XX transgenic animal (e.g. a fish, insect, reptile, amphibian, arachnid, or
XX mammal) by introducing (II) by cell fusion, lipid-mediated transfection
XX by a carrier system, microinjection, microcell fusion, electroporation,
XX microprojectile bombardment or direct DNA transfer into an embryonic
XX cell, preferably a stem cell or an embryo. (II) comprises a heterologous
XX nucleic acid that encodes a therapeutic product which is useful for
XX making a library of ACes comprising random portions of a genome. ACC44612
XX to ACC44732 and ABP96650 to ABP96657 represent sequences used in the
XX exemplification of the present invention
XX
XX Sequence 4346 BP; 1022 A; 1208 C; 1094 G; 1022 T; 0 U; 0 Other;
XX
XX Query Match 99.0%; Score 160.4; DB 7; Length 4346;
XX Best Local Similarity 99.4%; Pred. No. 9.2e-25;
XX Matches 161; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
XX 1 TCTGTTACAGTCTACTATACCATCTAGTGTAGTTCATCTAGTACGTGCATATGTTGTG 60
XX
XX 4070 TCTGTTACAGTCTACTATACCATCTAGTGTAGTTCATCTAGTACGTGCATATGTTGTG 4129
XX
XX 61 TTTTACAGTATTATGAGTCTGTTTTTTTATGCAAAATCTAATTTAATATATGATTTTA 120
XX
XX 4130 TTTTACAGTATTATGAGTCTGTTTTTTTATGCAAAATCTAATTTAATATATGATTTTA 4189
XX
XX 121 TATCATTTTACGTTTCTCGTCAGCTTTTTTATACATACTGTTG 162

DB 4190 TATCATTTTACGTTTCTCGTCAGCTTTTTTATACATACTGTTG 4231
|||||
RESULT 11
ABT16615
ID ABT16615 standard; DNA; 4346 BP.
XX
AC ABT16615;
XX
DT 03-APR-2003 (first entry)
XX
DE Artificial plant chromosome related plasmid DNA SEQ ID NO 26.
XX
KW Plant artificial chromosome; PAC; transgenic plant; vaccine;
KW blood factor; herbicide; stress; agronomical; nutrient quality;
KW bacterial artificial chromosome; BAC; yeast artificial chromosome; YAC;
KW ds.
XX
XX Unidentified.
XX OS
XX WO200296923-A1.
XX
XX 05-DEC-2002.
XX
XX 30-MAY-2002; 2002WO-US017451.
XX
XX 30-MAY-2001; 2001US-0294687P.
XX 04-JUN-2001; 2001US-0296329P.
XX
XX (CHRO-) CHROMOS MOLECULAR SYSTEMS INC.
XX PA
XX (AGRI-) AGRISOMA INC.
XX
XX Perez C, Fabijanski SF, Perkins E;
XX
XX WPI; 2003-140436/13.
XX
XX Producing artificial chromosome by introducing a nucleic acid into plant
XX cell, selecting artificial chromosome that has one or more repeat regions
XX PT with equivalent amounts of euchromatic and heterochromatic nucleic acids.
XX
XX Example 13; Page 255-256; 269pp; English.
XX
XX The invention relates to a novel method for producing plant artificial
XX chromosomes. The invention also relates to methods for targeting
XX insertion of heterologous DNA into plant artificial chromosomes, methods
XX for delivery of plant chromosomes to selected cells and tissues. The
XX isolated plant artificial chromosome (PAC) is useful for producing a
XX transgenic plant, which involves introducing the PAC into a plant cell.
XX The PAC comprises a heterologous nucleic acid encoding a gene product
XX such as enzymes, antisense RNA, rRNA, tRNA, structural proteins, marker
XX proteins, ligands, receptors, ribozymes, therapeutic proteins, and
XX biopharmaceutical proteins, vaccines, blood factors, antigens, hormones,
XX cytokines, growth factors, antibodies, or a product that provides for
XX resistance to diseases, insects, herbicides, or stress in a plant. The
XX heterologous nucleic acid optionally encodes a product that provides an
XX agronomically important trait in the plant, e.g. a product that alters
XX nutrient use and/or improves the nutrient quality of the plant. The
XX heterologous nucleic acid is contained within a bacterial artificial
XX chromosome (BAC) or a yeast artificial chromosome (YAC). This
XX polynucleotide sequence represents the DNA of a plasmid used in the
XX method of the invention
XX
XX Sequence 4346 BP; 1022 A; 1208 C; 1094 G; 1022 T; 0 U; 0 Other;
XX
XX Query Match 99.0%; Score 160.4; DB 7; Length 4346;
XX Best Local Similarity 99.4%; Pred. No. 9.2e-25;
XX Matches 161; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
XX 1 TCTGTTACAGTCTACTATACCATCTAGTGTAGTTCATCTAGTACGTGCATATGTTGTG 60
XX
XX 4070 TCTGTTACAGTCTACTATACCATCTAGTGTAGTTCATCTAGTACGTGCATATGTTGTG 4129
XX
XX 61 TTTTACAGTATTATGAGTCTGTTTTTTTATGCAAAATCTAATTTAATATATGATTTTA 120
XX
XX 4130 TTTTACAGTATTATGAGTCTGTTTTTTTATGCAAAATCTAATTTAATATATGATTTTA 4189
XX
XX 121 TATCATTTTACGTTTCTCGTCAGCTTTTTTATACATACTGTTG 162

QY 61 TTTTACAGTATTATGTAGTCTGTTTTTATGCAAAATCTAAATTAATATATGATATTTA 120
 |||||
 Db 4130 TTTTACAGTATTATGTAGTCTGTTTTTATGCAAAATCTAAATTAATATATGATATTTA 4189
 |||||

QY 121 TATCATTTTACGTTCTCGTTTCAGTTTCAGTTTATATATACTAACTTGG 162
 |||||
 Db 4190 TATCATTTTACGTTCTCGTTTCAGTTTATATATACTAACTTGG 4231
 |||||

RESULT 12
 AAT18924/C
 ID AAT18924 standard; DNA; 4909 BP.
 XX
 AC AAT18924;
 XX
 DT 17-JAN-1997 (first entry)
 XX
 DE Plasmid pA126i.
 XX
 KW Spider; dragline protein; variant; monomer; polymer; circular;
 fibre forming region; Spidroin 1; Nephila clavipes; Dp1; mimic;
 DP-1A analogue; fibre; high tensile strength; elasticity; clothing; rope;
 KW surgical suture; implant; reinforcement; film; coating; ss.
 XX
 OS Synthetic.
 XX
 FN WO9429450-A2.
 XX
 PD 22-DEC-1994.
 XX
 PF 15-JUN-1994; 94WO-US006689.
 XX
 PR 15-JUN-1993; 93US-00077600.
 XX
 PA (DUPO) DU PONT DE NEMOURS & CO E. I.
 XX
 PI Fahnstock SR;
 XX
 DR WPI; 1995-036479/05.
 XX

PT New synthetic variants of spider dragline protein - for making fibres
 useful as clothing, surgical silk, plastic reinforcement etc., also
 related DNA, vectors and transformed cells.
 PT
 PS Example 1; Fig 13; 168pp; English.
 XX

CC This sequence represents the complete nucleotide sequence of the plasmid
 pA126i. This plasmid was used in the construction of the vector pPS10
 which was used to express synthetic spider dragline variants, DP-1A.9 and
 DP-1B.9. pA126i comprises a replication origin active in *E. coli*, a
 selectable genetic marker which is a gene conferring resistance to
 ampicillin, sites for the restriction endonucleases BamHI and BglII with
 no essential sequences between them, and a third restriction site for
 PstI, located within the selectable marker which produces cohesive ends
 incompatible with those produced by BamHI and BglII. The polypeptide
 monomers are variants based on a consensus sequence derived from the
 fibre forming regions of spider dragline protein, esp. the natural
 protein 1 (Spidroin 1) from *Nephila clavipes*. Synthetic analogues of Dp1
 were designed to mimic the repeating consensus sequence of the natural
 protein and the pattern of variation among individual repeats. DP-1A
 analogues are composed of a tandemly repeated 101 amino acid monomer
 which comprises four repeats which differ from the consensus sequence
 given in AAW06201, according to the pattern (1)-(5): (1) the poly-alanine
 sequence varies in length from 0-7 residues; (2) when the entire poly-
 alanine sequence is deleted, so also is the surrounding sequence
 encompassing AGRGGLGGGAGAGG; (3) aside from the poly-alanine sequence,
 deletions usually encompass integral multiples of three consecutive
 residues; (4) deletion of GYG is generally accompanied by deletion of GRG
 in the same sequence; and (5) a repeat in which the entire poly-alanine
 sequence is deleted is generally preceded by a repeat containing six
 alanine residues. The proteins may be used to produce fibres of high
 tensile strength and elasticity, suitable for clothing, rope, surgical
 sutures, biomaterials for implants, plastic reinforcements, films,

CC coatings, etc
 XX
 SQ Sequence 4909 BP; 1216 A; 1251 C; 1258 G; 1184 T; 0 U; 0 Other;
 Query Match 99.0%; Score 160.4; DB 2; Length 4909;
 Best Local Similarity 99.4%; Pred. No. 9.2e-25;
 Matches 161; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TCTGTTACAGGTCACTAATACCATCTAAAGTAGTTGATTCATAGTACTGCATATGTTGTG 60
 |||||
 Db 2516 TCTGTTACAGGTCACTAATACCATCTAAAGTAGTTGATTCATAGTACTGCATATGTTGTG 2457
 |||||

QY 61 TTTTACAGTATTATGTAGTCTGTTTTTATGCAAAATCTAAATTAATATATGATATTTA 120
 |||||
 Db 2456 TTTTACAGTATTATGTAGTCTGTTTTTATGCAAAATCTAAATTAATATATGATATTTA 2397
 |||||

QY 121 TATCATTTTACGTTCTCGTTTCAGTTTATATATACTAACTTGG 162
 |||||
 Db 2396 TATCATTTTACGTTCTCGTTTCAGTTTATATATACTAACTTGG 2355
 |||||

RESULT 13
 AAF30800
 ID AAF30800 standard; DNA; 5641 BP.
 XX
 AC AAF30800;
 XX
 DT 11-SEP-2003 (revised)
 DT 21-JUN-2001 (first entry)
 XX
 DE Vector plasmid pJMF3 encoding LacZ-chitobiase fusion.
 XX
 KW Chitobiase; reporter gene; LacZ gene; promoter; vector; pJMF3; ds.
 XX
 OS Escherichia coli.
 OS Vibrio harveyi.
 OS Bacteriophage lambda.
 OS Chimeric.
 XX

Key Location/Qualifiers
 FT protein_bind 1783..1810
 FT /tag= a
 FT /note= "CAP-cAMP binding site"
 FT -35_signal 1820..1826
 FT /*tag= b
 FT -10_signal 1845..1850
 FT /function= "Lac promoter"
 FT /tag= c
 FT protein_bind 1857..1883
 FT /function= "Lac promoter"
 FT /tag= d
 FT CDS 1895..2014
 FT /note= "Lac repressor binding site"
 FT /*tag= e
 FT /partial
 FT /product= "lacZ-chitobiase fusion"
 XX
 WO200127322-A2.
 XX
 PD 19-APR-2001.
 XX
 PF 02-AUG-2000; 2000WO-US021048.
 XX
 PR 13-OCT-1999; 99US-0159221P.
 XX
 PA (ELIT-) ELITRA PHARM INC.
 XX
 PI Zyskind J;
 XX
 DR WPI; 2001-290731/30.
 DR P-PSDB; AAB20484.
 XX
 PT Identifying a regulatory element capable of directing or regulating

transcription (e.g. a promoter) comprises providing a construct linked to a nucleic acid encoding a cytoplasmic form of chitinase.

Example 1; Page 32-34; 44pp; English.

The present sequence is that of vector plasmid pJMF3, which includes phage lambda attP and the lac promoter with the first 21 amino acids of lacZ-alpha (from plasmid pUC19) fused in-frame to the *Vibrio harveyi* chitinase gene (see AAB20484). The invention relates to genetic constructs and methods of using a cytoplasmic form of chitinase enzyme as a reporter. A claimed reporter gene construct comprises pJMF3. The invention also comprises expression vectors which express the cytoplasmic form of chitinase. Methods are provided for: characterizing a promoter; identifying a regulatory element capable of directing and regulating transcription within a test sequence; detecting a successful transformation; and for monitoring the activity of a promoter. Chitinase has an advantage over beta-galactosidase as a reporter gene in that it is not necessary to engineer many host cells to lack reporter activity. (Updated on 11-SEP-2003 to standardise OS field)

Sequence 5641 BP; 1539 A; 1305 C; 1336 G; 1461 T; 0 U; 0 Other;

Query Match 99.0%; Score 160.4; DB 4; Length 5641;
Best Local Similarity 99.4%; Pred. No. 9.2e-25;
Matches 161; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TCTGTTACAGGTCACATAACCATCTAAGTAGTTCGATTCATAGTCGACATGCTGTTG 60
|||||
Db 4703 TCTGTTACAGGTCACATAACCATCTAAGTAGTTCGATTCATAGTCGACATGCTGTTG 4762

QY 61 TTTTACAGTATTATGTCGTCGTTTTTATGCAAAATCTAATTTAATATATTGATTTTA 120
|||||
Db 4763 TTTTACAGTATTATGTCGTCGTTTTTATGCAAAATCTAATTTAATATATTGATTTTA 4822

QY 121 TATCATTTTACGTTTCTCGTCGACGTTTTTATACAACTTG 162
|||||
Db 4823 TATCATTTTACGTTTCTCGTCGACGTTTTTATACAACTTG 4864

RESULT 14
AAF30801/c
ID AAF30801 standard; DNA; 5670 BP.

AC AAF30801;

XX 11-SEP-2003 (revised)
DT 21-JUN-2001 (first entry)

Vector plasmid pJMF4 encoding LacZ-chitinase fusion.

Chitinase; reporter gene; LacZ gene; promoter; vector; pJMF4; ds.

Escherichia coli.

Vibrio harveyi.

Bacteriophage lambda.

Chimeric.

Key Location/Qualifiers
FT protein_bind 1783..1810
FT /*tag= a
FT /note= "CAP-cAMP binding site"
FT -35_signal 1820..1826
FT /*tag= b
FT -10_signal 1845..1850
FT /function= "Lac promoter"
FT /*tag= c
FT protein_bind 1857..1883
FT /function= "Lac promoter"
FT /*tag= d
FT /note= "Lac repressor binding site"
FT CDS 1895..2014
FT /*tag= e
FT /partial

/product= "lacZ-chitinase fusion"

WO200127322-A2.

19-APR-2001.

02-AUG-2000; 2000WO-US021048.

13-OCT-1999; 99US-0159221P.

(ELIT-) ELITRA PHARM INC.

Zyskind J;

WPI; 2001-290731/30.

P-PSDB; AAB20484.

Identifying a regulatory element capable of directing or regulating transcription (e.g. a promoter) comprises providing a construct linked to a nucleic acid encoding a cytoplasmic form of chitinase.

Example 1; Page 34-36; 44pp; English.

The present sequence is that of vector plasmid pJMF4, which includes phage lambda attP and the lac promoter with the first 21 amino acids of lacZ-alpha (from plasmid pUC19) fused in-frame to the *Vibrio harveyi* chitinase gene (see AAB20484). The invention relates to genetic constructs and methods of using a cytoplasmic form of chitinase enzyme as a reporter. A claimed reporter gene construct comprises pJMF4. The invention also comprises expression vectors which express the cytoplasmic form of chitinase. Methods are provided for: characterizing a promoter; identifying a regulatory element capable of directing and regulating transcription within a test sequence; detecting a successful transformation; and for monitoring the activity of a promoter. Chitinase has an advantage over beta-galactosidase as a reporter gene in that it is not necessary to engineer many host cells to lack reporter activity. (Updated on 11-SEP-2003 to standardise OS field)

Sequence 5670 BP; 1567 A; 1302 C; 1356 G; 1445 T; 0 U; 0 Other;

Query Match 99.0%; Score 160.4; DB 4; Length 5670;
Best Local Similarity 99.4%; Pred. No. 9.2e-25;
Matches 161; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TCTGTTACAGGTCACATAACCATCTAAGTAGTTCGATTCATAGTCGACATGCTGTTG 60
|||||
Db 5041 TCTGTTACAGGTCACATAACCATCTAAGTAGTTCGATTCATAGTCGACATGCTGTTG 4982

QY 61 TTTTACAGTATTATGTCGTCGTTTTTATGCAAAATCTAATTTAATATATTGATTTTA 120
|||||
Db 4981 TTTTACAGTATTATGTCGTCGTTTTTATGCAAAATCTAATTTAATATATTGATTTTA 4922

QY 121 TATCATTTTACGTTTCTCGTCGACGTTTTTATACAACTTG 162
|||||
Db 4921 TATCATTTTACGTTTCTCGTCGACGTTTTTATACAACTTG 4880

RESULT 15
AAF30798
ID AAF30798 standard; DNA; 5826 BP.

AC AAF30798;

DT 11-SEP-2003 (revised)
DT 21-JUN-2001 (first entry)

Vector plasmid pJMF6 encoding chitinase reporter enzyme.

Chitinase; reporter gene; dnaA gene; promoter; vector; pJMF6; ds.

Escherichia coli.

Vibrio harveyi.

Chimeric.

[illegible]

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: September 9, 2004, 19:34:38 ; Search time 128.856 Seconds
(without alignments)
3982.858 Million cell updates/sec

Title: US-10-082-772B-3

Perfect score: 102

Sequence: 1 ctgctttttatactaagtt.....taaaatcatattgatttc 102

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 3304383 seqs, 2515761380 residues

Total number of hits satisfying chosen parameters: 6608766

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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2: /cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq.*
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19: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	102	100.0	102	17	US-10-310-695-15
2	102	100.0	105	17	US-10-627-711-9
3	102	100.0	108	13	US-10-403-232-174
4	102	100.0	3049	13	US-10-432-148-4
5	102	100.0	5349	9	US-09-970-921-7
6	102	100.0	5611	9	US-09-970-921-10
7	100.4	98.4	243	13	US-10-403-232-173
8	100.4	98.4	243	17	US-10-310-695-2
9	100.4	98.4	243	17	US-10-310-695-14
10	100.4	98.4	248	17	US-10-627-711-8
11	100.4	98.4	282	15	US-10-627-711-9
12	100.4	98.4	1763	11	US-09-244-805-57
13	100.4	98.4	1763	11	US-09-245-277-57
14	100.4	98.4	1763	17	US-10-792-481-57

15	100.4	98.4	2959	13	US-10-270-176-8	Sequence 8, Appli
16	100.4	98.4	3663	13	US-10-270-176-3	Sequence 3, Appli
17	100.4	98.4	3695	13	US-10-270-176-13	Sequence 13, Appl
18	100.4	98.4	4346	15	US-10-161-403-113	Sequence 113, App
19	100.4	98.4	4782	13	US-10-270-176-20	Sequence 20, Appl
20	100.4	98.4	5646	13	US-10-270-176-39	Sequence 39, Appl
21	100.4	98.4	5646	13	US-10-270-176-41	Sequence 41, Appl
22	100.4	98.4	5706	13	US-10-270-176-40	Sequence 40, Appl
23	100.4	98.4	5739	13	US-10-270-176-9	Sequence 9, Appli
24	100.4	98.4	5771	13	US-10-270-176-34	Sequence 34, Appl
25	100.4	98.4	5771	13	US-10-270-176-35	Sequence 35, Appl
26	100.4	98.4	5814	13	US-10-270-176-37	Sequence 37, Appl
27	100.4	98.4	5911	13	US-10-270-176-42	Sequence 42, Appl
28	100.4	98.4	5929	13	US-10-270-176-45	Sequence 45, Appl
29	100.4	98.4	5929	13	US-10-270-176-46	Sequence 46, Appl
30	100.4	98.4	5948	13	US-10-270-176-21	Sequence 21, Appl
31	100.4	98.4	5986	13	US-10-270-176-36	Sequence 36, Appl
32	100.4	98.4	6200	13	US-10-270-176-38	Sequence 38, Appl
33	100.4	98.4	6664	13	US-10-270-176-1	Sequence 1, Appli
34	100.4	98.4	6668	13	US-10-270-176-2	Sequence 2, Appli
35	100.4	98.4	6742	13	US-10-270-176-19	Sequence 19, Appl
36	100	98.0	119	10	US-09-981-803-12	Sequence 12, Appl
37	93.8	92.0	100	13	US-10-301-849A-17	Sequence 17, Appl
38	93.8	92.0	1688	16	US-10-374-780A-393	Sequence 393, App
39	93.8	92.0	2717	15	US-10-151-690-18	Sequence 18, Appl
40	92.2	90.4	100	13	US-10-403-232-180	Sequence 180, App
41	92.2	90.4	659	15	US-10-349-782-9	Sequence 9, Appli
42	92.2	90.4	2591	15	US-10-005-876A-70	Sequence 70, Appl
43	92.2	90.4	2607	15	US-10-005-876A-71	Sequence 71, Appl
44	92.2	90.4	2831	15	US-10-241-596-133	Sequence 133, App
45	92.2	90.4	3647	15	US-10-241-596-134	Sequence 134, App

ALIGNMENTS

RESULT 1
US-10-310-695-15
; Sequence 15, Application US/10310695
; Publication No. US20040110293A1
; GENERAL INFORMATION:
; APPLICANT: DROGE, PETER
; APPLICANT: ENENKEL, BARBARA
; TITLE OF INVENTION: SEQUENCE SPECIFIC DNA RECOMBINATION IN EUKARYOTIC CELLS
; FILE REFERENCE: DEBE:0190S
; CURRENT APPLICATION NUMBER: US/10/310,695
; CURRENT FILING DATE: 2002-12-05
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 15
; LENGTH: 102
; TYPE: DNA
; ORGANISM: Escherichia coli
US-10-310-695-15

Query Match 100.0%; Score 102; DB 17; Length 102;
Best Local Similarity 100.0%; Pred. No. 1.6e-18;
Matches 102; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 CTGCTTTTATCTAAGTTGGCATTATAAAAAGCATTGCTTATCAATTGTTGCAACG 60
Qy 61 AACAGGTCATCATCAGTCAAAAATAAATCATTTATTGATTTC 102
Db 61 AACAGGTCATCATCAGTCAAAAATAAATCATTTATTGATTTC 102

RESULT 2
US-10-627-711-9
; Sequence 9, Application US/10627711
; Publication No. US20040115812A1
; GENERAL INFORMATION:

```
; APPLICANT: YANG, Shuwei
; TITLE OF INVENTION: METHODS AND NUCLEIC ACID VECTORS FOR RAPID EXPRESSION AND
; FILE REFERENCE: 51236US
; CURRENT APPLICATION NUMBER: US/10/627,711
; CURRENT FILING DATE: 2003-07-28
; PRIOR APPLICATION NUMBER: 60/398,589
; PRIOR FILING DATE: 2002-07-26
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 9
; LENGTH: 105
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: primer
US-10-627-711-9

Query Match          100.0%; Score 102; DB 17; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.6e-18;
Matches 102; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTGCTTTTATCTAAGTTGGCATTATATAAAGCAATGCTTATCAATTGTTGCAACG 60
Db 4 CTGCTTTTATCTAAGTTGGCATTATATAAAGCAATGCTTATCAATTGTTGCAACG 63

QY 61 AACAGTCACTATCAGTCAAAATAAAATCAATTATTGATTC 102
Db 64 AACAGTCACTATCAGTCAAAATAAAATCAATTATTGATTC 105

RESULT 3
US-10-403-232-174
; Sequence 174, Application US/10403232
; Publication No. US20030226164A1
; GENERAL INFORMATION:
; APPLICANT: Suttie, Janet Louise
; APPLICANT: Chilton, Mary-Dell
; APPLICANT: Que, Qindeng
; APPLICANT: de Framond, Anic
; TITLE OF INVENTION: Lambda Integrase Mediated Recombination In Plants
; FILE REFERENCE: 70005USPS
; CURRENT APPLICATION NUMBER: US/10/403,232
; CURRENT FILING DATE: 2003-03-28
; NUMBER OF SEQ ID NOS: 185
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 174
; LENGTH: 108
; TYPE: DNA
; ORGANISM: Bacteriophage lambda
US-10-403-232-174

Query Match          100.0%; Score 102; DB 13; Length 108;
Best Local Similarity 100.0%; Pred. No. 1.6e-18;
Matches 102; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTGCTTTTATCTAAGTTGGCATTATATAAAGCAATGCTTATCAATTGTTGCAACG 60
Db 7 CTGCTTTTATCTAAGTTGGCATTATATAAAGCAATGCTTATCAATTGTTGCAACG 66

QY 61 AACAGTCACTATCAGTCAAAATAAAATCAATTATTGATTC 102
Db 67 AACAGTCACTATCAGTCAAAATAAAATCAATTATTGATTC 108

RESULT 4
US-10-432-148-4
; Sequence 4, Application US/10432148
; Publication No. US20040064853A1
; GENERAL INFORMATION:
; APPLICANT: KWS SAAT AG
; TITLE OF INVENTION: tissue specific promoter
; FILE REFERENCE: tissue specific promoter 1
```

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; CURRENT APPLICATION NUMBER: US/10/432,148
; CURRENT FILING DATE: 2003-05-16
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 3049
; TYPE: DNA
; ORGANISM: Beta vulgaris
; FEATURE:
; NAME/KEY: promoter
; LOCATION: (1)..(2998)
; FEATURE:
; NAME/KEY: mRNA
; LOCATION: (2928)..(3049)
; FEATURE:
; NAME/KEY: TATA signal
; LOCATION: (2877)..(2883)
US-10-432-148-4

Query Match          100.0%; Score 102; DB 13; Length 3049;
Best Local Similarity 100.0%; Pred. No. 5.1e-18;
Matches 102; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTGCTTTTATCTAAGTTGGCATTATATAAAGCAATGCTTATCAATTGTTGCAACG 60
Db 2398 CTGCTTTTATCTAAGTTGGCATTATATAAAGCAATGCTTATCAATTGTTGCAACG 2457

QY 61 AACAGTCACTATCAGTCAAAATAAAATCAATTATTGATTC 102
Db 2458 AACAGTCACTATCAGTCAAAATAAAATCAATTATTGATTC 2499

RESULT 5
US-09-970-921-7/c
; Sequence 7, Application US/09970921
; Patent No. US20020133845A1
; GENERAL INFORMATION:
; APPLICANT: Frank Michiels et al.
; TITLE OF INVENTION: Improved Barstar Gene
; FILE REFERENCE: 2428-0108P
; CURRENT APPLICATION NUMBER: US/09/970,921
; CURRENT FILING DATE: 2001-10-05
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 7
; LENGTH: 5349
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: other nucleic
; OTHER INFORMATION: acid, "T-DNA of pTTS243"
; NAME/KEY: misc feature
; LOCATION: Complement((1)..(25))
; OTHER INFORMATION: label = RB, "T-DNA right border"
; NAME/KEY: misc feature
; LOCATION: Complement((98)..(331))
; OTHER INFORMATION: label = 3'g7, "region containing 3' untranslated
; OTHER INFORMATION: end of Agrobacterium T-DNA gene 7"
; NAME/KEY: misc feature
; LOCATION: Complement((332)..(883))
; OTHER INFORMATION: label = bar, "region coding for phosphinotricin
; OTHER INFORMATION: acetyl transferase"
; NAME/KEY: misc feature
; LOCATION: Complement((884)..(2258))
; OTHER INFORMATION: label = P35S, "35S promoter of Cauliflower Mosaic
; OTHER INFORMATION: Virus"
; NAME/KEY: misc feature
; LOCATION: (2281)..(3969)
; OTHER INFORMATION: label = PE1, "promoter of E1 gene of rice (WO
; OTHER INFORMATION: 92/13956)"
; NAME/KEY: misc feature
; LOCATION: (3970)..(4245)
; OTHER INFORMATION: label = synb*, "improved barstar DNA"
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/ NAME/KEY: misc feature
/ LOCATION: (4246)..(4577)
/ OTHER INFORMATION: label = 3'chs, "region containing 3' untranslated
/ OTHER INFORMATION: end of chalcone synthase gene"
/ NAME/KEY: misc feature
/ LOCATION: Complement((5325)..(5349))
/ OTHER INFORMATION: label = LB, "T-DNA left border"
US-09-970-921-7
Query Match 100.0%; Score 102; DB 9; Length 5349;
Best Local Similarity 100.0%; Pred. No. 6.2e-18;
Matches 102; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTGCTTTTATCTAAGTTGGCATTATATAAAAGCAATTCCTTATCAATTTGTTGCAACG 60
Db 4885 CTGCTTTTATCTAAGTTGGCATTATATAAAAGCAATTCCTTATCAATTTGTTGCAACG 4826

QY 61 AACAGTCACTATCAGTCAAAATATAAATCAATTTGATTTC 102
Db 4825 AACAGTCACTATCAGTCAAAATATAAATCAATTTGATTTC 4784

RESULT 6
US-09-970-921-10/c
/ Sequence 10, Application US/09970921
/ Patent No. US20020133845A1
/ GENERAL INFORMATION:
/ APPLICANT: Frank Michiels et al.
/ TITLE OF INVENTION: Improved Barstar Gene
/ FILE REFERENCE: 2428-0108P
/ CURRENT APPLICATION NUMBER: US/09/970,921
/ CURRENT FILING DATE: 2001-10-05
/ NUMBER OF SEQ ID NOS: 10
/ SOFTWARE: PatentIn Ver. 2.0
/ SEQ ID NO 10
/ LENGTH: 5611
/ TYPE: DNA
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence: other nucleic
/ OTHER INFORMATION: acid, "plasmid pLH48"
/ NAME/KEY: misc feature
/ LOCATION: Complement((39)..(317))
/ OTHER INFORMATION: label = 3'nos, "region containing 3' untranslated
/ OTHER INFORMATION: end of nopaline synthase gene of Agrobacterium
/ OTHER INFORMATION: T-DNA"
/ NAME/KEY: misc feature
/ LOCATION: Complement((318)..(869))
/ OTHER INFORMATION: label = bar, "region coding for phosphinothricin
/ OTHER INFORMATION: acetyl transferase"
/ NAME/KEY: misc feature
/ LOCATION: Complement((870)..(1702))
/ OTHER INFORMATION: label = P35S, "35S promoter of Cauliflower Mosaic
/ OTHER INFORMATION: Virus"
/ NAME/KEY: misc feature
/ LOCATION: (1740)..(2284)
/ OTHER INFORMATION: label = PTA29, "promoter of TA29 gene of Nicotiana
/ OTHER INFORMATION: tabacum"
/ NAME/KEY: misc feature
/ LOCATION: (2285)..(2560)
/ OTHER INFORMATION: label = synb+, "improved barstar DNA"
/ NAME/KEY: misc feature
/ LOCATION: (2561)..(2892)
/ OTHER INFORMATION: label = 3'chs, "region containing 3' untranslated
/ OTHER INFORMATION: end of chalcone synthase gene"
US-09-970-921-10
Query Match 100.0%; Score 102; DB 9; Length 5611;
Best Local Similarity 100.0%; Pred. No. 6.3e-18;
Matches 102; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTGCTTTTATCTAAGTTGGCATTATATAAAAGCAATTCCTTATCAATTTGTTGCAACG 60
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Db 3200 CTGCTTTTATCTAAGTTGGCATTATATAAAAGCAATTCCTTATCAATTTGTTGCAACG 3141

QY 61 AACAGTCACTATCAGTCAAAATATAAATCAATTTGATTTC 102
Db 3140 AACAGTCACTATCAGTCAAAATATAAATCAATTTGATTTC 3099

RESULT 7
US-10-403-232-173
/ Sequence 173, Application US/10403232
/ Publication No. US20030226164A1
/ GENERAL INFORMATION:
/ APPLICANT: Suttie, Janet Louise
/ APPLICANT: Chilton, Mary-Dell
/ APPLICANT: Que, Quideng
/ TITLE OF INVENTION: Lambda Integrase Mediated Recombination In Plants
/ FILE REFERENCE: 70005USPS
/ CURRENT APPLICATION NUMBER: US/10/403,232
/ CURRENT FILING DATE: 2003-03-28
/ NUMBER OF SEQ ID NOS: 185
/ SOFTWARE: PatentIn version 3.2
/ SEQ ID NO 173
/ LENGTH: 243
/ TYPE: DNA
/ ORGANISM: Bacteriophage lambda
US-10-403-232-173
Query Match 98.4%; Score 100.4; DB 13; Length 243;
Best Local Similarity 99.0%; Pred. No. 5.9e-18;
Matches 101; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CTGCTTTTATCTAAGTTGGCATTATATAAAAGCAATTCCTTATCAATTTGTTGCAACG 60
Db 142 CAGCTTTTATCTAAGTTGGCATTATATAAAAGCAATTCCTTATCAATTTGTTGCAACG 201

QY 61 AACAGTCACTATCAGTCAAAATATAAATCAATTTGATTTC 102
Db 202 AACAGTCACTATCAGTCAAAATATAAATCAATTTGATTTC 243

RESULT 8
US-10-310-695-2
/ Sequence 2, Application US/10310695
/ Publication No. US20040110293A1
/ GENERAL INFORMATION:
/ APPLICANT: DROGE, PETER
/ APPLICANT: ENENKEL, BARBARA
/ TITLE OF INVENTION: SEQUENCE SPECIFIC DNA RECOMBINATION IN EUKARYOTIC CELLS
/ FILE REFERENCE: DBEE.019US
/ CURRENT APPLICATION NUMBER: US/10/310,695
/ CURRENT FILING DATE: 2002-12-05
/ NUMBER OF SEQ ID NOS: 22
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 2
/ LENGTH: 243
/ TYPE: DNA
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-10-310-695-2
Query Match 98.4%; Score 100.4; DB 17; Length 243;
Best Local Similarity 99.0%; Pred. No. 5.9e-18;
Matches 101; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CTGCTTTTATCTAAGTTGGCATTATATAAAAGCAATTCCTTATCAATTTGTTGCAACG 60
Db 142 CAGCTTTTATCTAAGTTGGCATTATATAAAAGCAATTCCTTATCAATTTGTTGCAACG 201

QY 61 AACAGTCACTATCAGTCAAAATATAAATCAATTTGATTTC 102
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Db 202 AACAGGTCATCATAGTCAAAATAAAATCAATTATTGATTC 243

RESULT 9

US-10-310-695-14
; Sequence 14, Application US/10310695
; Publication No. US20040110293A1
; GENERAL INFORMATION:
; APPLICANT: DROGE, PETER
; APPLICANT: ENENKEL, BARBARA
; TITLE OF INVENTION: SEQUENCE SPECIFIC DNA RECOMBINATION IN EUKARYOTIC CELLS
; FILE REFERENCE: DEB:019US
; CURRENT APPLICATION NUMBER: US/10/310,695
; CURRENT FILING DATE: 2002-12-05
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 14
; LENGTH: 243
; TYPE: DNA
; ORGANISM: Bacteriophage lambda
US-10-310-695-14

Query Match 98.4%; Score 100.4; DB 17; Length 243;
Best Local Similarity 99.0%; Pred. No. 5.9e-18;
Matches 101; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 CTGCTTTTATCTAAGTTGGCATTATATAAAAGCATTCGTTATCAATTTGTTGCAACG 60
Db 142 CAGCTTTTATCTAAGTTGGCATTATATAAAAGCATTCGTTATCAATTTGTTGCAACG 201
QY 61 AACAGGTCATCATAGTCAAAATAAAATCAATTATTGATTC 102
Db 202 AACAGGTCATCATAGTCAAAATAAAATCAATTATTGATTC 243

RESULT 10

US-10-627-711-8
; Sequence 8, Application US/10627711
; Publication No. US20040115812A1
; GENERAL INFORMATION:
; APPLICANT: YANG, Shuwei
; TITLE OF INVENTION: METHODS AND NUCLEIC ACID VECTORS FOR RAPID EXPRESSION AND
; FILE REFERENCE: SCREENING OF CDNA CLONES
; FILE REFERENCE: 51236US
; CURRENT APPLICATION NUMBER: US/10/627,711
; CURRENT FILING DATE: 2003-07-28
; PRIOR APPLICATION NUMBER: 60/398,589
; PRIOR FILING DATE: 2002-07-26
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 8
; LENGTH: 248
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: primer
US-10-627-711-8

Query Match 98.4%; Score 100.4; DB 17; Length 248;
Best Local Similarity 99.0%; Pred. No. 6e-19;
Matches 101; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 CTGCTTTTATCTAAGTTGGCATTATATAAAAGCATTCGTTATCAATTTGTTGCAACG 60
Db 147 CAGCTTTTATCTAAGTTGGCATTATATAAAAGCATTCGTTATCAATTTGTTGCAACG 206
QY 61 AACAGGTCATCATAGTCAAAATAAAATCAATTATTGATTC 102
Db 207 AACAGGTCATCATAGTCAAAATAAAATCAATTATTGATTC 248

RESULT 11

US-10-161-403-72

; Sequence 72, Application US/10161403
; Publication No. US20030119104A1
; GENERAL INFORMATION:
; APPLICANT: Perkins, Edward
; APPLICANT: Perez, Carl
; APPLICANT: Lindenbaum, Michael
; APPLICANT: Greene, Amy
; APPLICANT: Leung, Josephine
; APPLICANT: Fleming, Elena
; APPLICANT: Stewart, Sandra
; APPLICANT: Shellard, Joan
; TITLE OF INVENTION: CHROMOSOME-BASED PLATFORMS
; FILE REFERENCE: 24601-420
; CURRENT APPLICATION NUMBER: US/10/161,403
; CURRENT FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: 60/294,758
; PRIOR FILING DATE: 2001-05-30
; PRIOR APPLICATION NUMBER: 60/366,891
; PRIOR FILING DATE: 2002-03-21
; NUMBER OF SEQ ID NOS: 129
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 72
; LENGTH: 282
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: attp
US-10-161-403-72
Query Match 98.4%; Score 100.4; DB 15; Length 282;
Best Local Similarity 99.0%; Pred. No. 6.2e-18;
Matches 101; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 CTGCTTTTATCTAAGTTGGCATTATATAAAAGCATTCGTTATCAATTTGTTGCAACG 60
Db 156 CAGCTTTTATCTAAGTTGGCATTATATAAAAGCATTCGTTATCAATTTGTTGCAACG 215
QY 61 AACAGGTCATCATAGTCAAAATAAAATCAATTATTGATTC 102
Db 216 AACAGGTCATCATAGTCAAAATAAAATCAATTATTGATTC 257
RESULT 12
US-09-244-805-57/c
; Sequence 57, Application US/09244805
; Publication No. US20030203840A1
; GENERAL INFORMATION:
; APPLICANT: Worley, Paul F.
; APPLICANT: Lanahan, Anthony
; APPLICANT: Goetz, Bernard
; APPLICANT: Helmisch, Holger
; APPLICANT: Kuner, Rohini
; APPLICANT: Scheek, Sigrid
; APPLICANT: Nikolic, Karoly
; APPLICANT: Zhukovski, Eugene
; TITLE OF INVENTION: IMMEDIATE EARLY GENES AND METHODS OF USE
; FILE REFERENCE: 10496/004001
; CURRENT APPLICATION NUMBER: US/09/244,805
; CURRENT FILING DATE: 1999-02-05
; EARLIER APPLICATION NUMBER: 60/074,518
; EARLIER FILING DATE: 1998-02-12
; EARLIER APPLICATION NUMBER: 60/074,135
; EARLIER FILING DATE: 1998-02-06
; NUMBER OF SEQ ID NOS: 62
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 57
; LENGTH: 1763
; TYPE: DNA
; ORGANISM: Eukaryote
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)...(1763)

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; OTHER INFORMATION: Y = C or T
; OTHER INFORMATION: n = A,T,C or G
US-09-244-805-57

Query Match      98.4%; Score 100.4; DB 11; Length 1763;
Best Local Similarity 99.0%; Pred. No. 1.2e-17;
Matches 101; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CTGCTTTTATCTAAGTTGGCATTATAAAAAGCATTGCTTATCAATTGTTGCAACG 60
Db 290 CAGCTTTTATCTAAGTTGGCATTATAAAAAGCATTGCTTATCAATTGTTGCAACG 231

QY 61 AACAGGTCACCTATCAGTCAAAATAAAATCAATTATTGATTTC 102
Db 230 AACAGGTCACCTATCAGTCAAAATAAAATCAATTATTGATTTC 189

RESULT 13
US-09-245-277-57/c
; Sequence 57, Application US/09245277
; Publication No. US20030211984A1
; GENERAL INFORMATION:
; APPLICANT: Worley, Paul F.
; APPLICANT: Lanahan, Anthony
; TITLE OF INVENTION: IMMEDIATE EARLY GENES AND METHODS OF USE
; FILE REFERENCE: JHU1530-3
; CURRENT APPLICATION NUMBER: US/09/245,277
; CURRENT FILING DATE: 1999-02-05
; PRIOR APPLICATION NUMBER: 60/074,518
; PRIOR FILING DATE: 1998-02-12
; PRIOR APPLICATION NUMBER: 60/074,135
; PRIOR FILING DATE: 1998-02-06
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 57
; LENGTH: 1763
; TYPE: DNA
; ORGANISM: Eukaryote
; NAME/KEY: misc_feature
; LOCATION: (1)...(1763)
; OTHER INFORMATION: Y = C or T
; OTHER INFORMATION: n = A,T,C or G
US-09-245-277-57

Query Match      98.4%; Score 100.4; DB 11; Length 1763;
Best Local Similarity 99.0%; Pred. No. 1.2e-17;
Matches 101; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CTGCTTTTATCTAAGTTGGCATTATAAAAAGCATTGCTTATCAATTGTTGCAACG 60
Db 290 CAGCTTTTATCTAAGTTGGCATTATAAAAAGCATTGCTTATCAATTGTTGCAACG 231

QY 61 AACAGGTCACCTATCAGTCAAAATAAAATCAATTATTGATTTC 102
Db 230 AACAGGTCACCTATCAGTCAAAATAAAATCAATTATTGATTTC 189

RESULT 14
US-10-792-481-57/c
; Sequence 57, Application US/10792481
; Publication No. US20040152658A1
; GENERAL INFORMATION:
; APPLICANT: Worley, Paul F.
; APPLICANT: Lanahan, Anthony
; APPLICANT: Goetz, Bernard
; APPLICANT: Heimsch, Holger
; APPLICANT: Kuner, Rohini
; APPLICANT: Scheek, Sigrud
; APPLICANT: Nikolich, Karoly
; APPLICANT: Zhukovski, Eugene
; TITLE OF INVENTION: IMMEDIATE EARLY GENES AND METHODS OF USE
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; TITLE OF INVENTION: THEREFOR
; FILE REFERENCE: 10496/004001
; CURRENT APPLICATION NUMBER: US/10/792,481
; CURRENT FILING DATE: 2004-03-02
; PRIOR APPLICATION NUMBER: US/09/244,805
; PRIOR FILING DATE: 1999-02-05
; PRIOR APPLICATION NUMBER: 60/074,518
; PRIOR FILING DATE: 1998-02-12
; PRIOR APPLICATION NUMBER: 60/074,135
; PRIOR FILING DATE: 1998-02-06
; NUMBER OF SEQ ID NOS: 62
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 57
; LENGTH: 1763
; TYPE: DNA
; ORGANISM: Eukaryote
; NAME/KEY: misc_feature
; LOCATION: (1)...(1763)
; OTHER INFORMATION: Y = C or T
; OTHER INFORMATION: n = A,T,C or G
US-10-792-481-57

Query Match      98.4%; Score 100.4; DB 17; Length 1763;
Best Local Similarity 99.0%; Pred. No. 1.2e-17;
Matches 101; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CTGCTTTTATCTAAGTTGGCATTATAAAAAGCATTGCTTATCAATTGTTGCAACG 60
Db 290 CAGCTTTTATCTAAGTTGGCATTATAAAAAGCATTGCTTATCAATTGTTGCAACG 231

QY 61 AACAGGTCACCTATCAGTCAAAATAAAATCAATTATTGATTTC 102
Db 230 AACAGGTCACCTATCAGTCAAAATAAAATCAATTATTGATTTC 189

RESULT 15
US-10-270-176-8
; Sequence 8, Application US/10270176
; Publication No. US20040033609A1
; GENERAL INFORMATION:
; APPLICANT: Wanner, Barry
; APPLICANT: Haldmann, Andreas
; TITLE OF INVENTION: PLASMIDS, STRAINS, AND METHODS OF USE
; FILE REFERENCE: 290.00140101
; CURRENT APPLICATION NUMBER: US/10/270,176
; CURRENT FILING DATE: 2002-10-10
; PRIOR APPLICATION NUMBER: 60/328,642
; PRIOR FILING DATE: 2001-10-10
; PRIOR APPLICATION NUMBER: 60/375,059
; PRIOR FILING DATE: 2002-04-24
; NUMBER OF SEQ ID NOS: 118
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 8
; LENGTH: 2959
; TYPE: DNA
; ORGANISM: artificial
; FEATURE:
; OTHER INFORMATION: CRIM plasmid
US-10-270-176-8

Query Match      98.4%; Score 100.4; DB 13; Length 2959;
Best Local Similarity 99.0%; Pred. No. 1.4e-17;
Matches 101; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CTGCTTTTATCTAAGTTGGCATTATAAAAAGCATTGCTTATCAATTGTTGCAACG 60
Db 1082 CAGCTTTTATCTAAGTTGGCATTATAAAAAGCATTGCTTATCAATTGTTGCAACG 1141

QY 61 AACAGGTCACCTATCAGTCAAAATAAAATCAATTATTGATTTC 102
Db 1142 AACAGGTCACCTATCAGTCAAAATAAAATCAATTATTGATTTC 1183
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Search completed: September 10, 2004, 00:14:08
Job time : 129.856 secs

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OM nucleic - nucleic search, using sw model

Run on: September 9, 2004, 17:33:11 ; Search time 35.7198 Seconds
(without alignments)
2516.866 Million cell updates/sec

Title: US-10-082-772B-4

Perfect score: 162
Sequence: 1 tctgtacaggtaactaata.....agctttttataacttg 162

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 682709 seqs, 277475446 residues

Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents NA:*

- 1: /cgn2_6/ptodata/2/ina/5A.COMB.seq.*
- 2: /cgn2_6/ptodata/2/ina/5B.COMB.seq.*
- 3: /cgn2_6/ptodata/2/ina/6A.COMB.seq.*
- 4: /cgn2_6/ptodata/2/ina/6B.COMB.seq.*
- 5: /cgn2_6/ptodata/2/ina/PTGUS.COMB.seq.*
- 6: /cgn2_6/ptodata/2/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	160.4	99.0	4909	3	US-08-556-978B-78
C 2	160.4	99.0	6043	4	US-09-630-929-4
C 3	160.4	99.0	7652	1	US-07-590-988A-1
4	104.6	64.6	38584	4	US-09-433-702B-50
5	97.4	60.1	200	1	US-08-021-667A-17
6	97.4	60.1	200	1	US-08-410-544-17
7	97.4	60.1	200	1	US-08-728-785A-17
8	67.8	41.9	9827	4	US-09-453-702B-66
9	61.4	37.9	201	1	US-08-021-667A-18
10	61.4	37.9	201	1	US-08-410-544-18
11	61.4	37.9	201	1	US-08-728-785A-18
12	39	24.1	640681	4	US-09-790-988-1
C 13	38.2	23.6	19124	2	US-08-487-826B-13
C 14	37.6	23.2	640681	4	US-09-790-988-1
C 15	37.4	23.1	7786	4	US-09-790-988-2
16	37.2	23.0	3078	4	US-09-601-198-54
17	36.4	22.5	5455	4	US-10-204-708-33
18	36.4	22.5	10467	4	US-10-204-708-2
19	36	22.2	1725	4	US-08-882-164D-31
20	36	22.2	6326	4	US-10-204-708-57
21	36	22.2	11131	4	US-10-204-708-27
22	35.8	22.1	6306	4	US-10-204-708-50
23	35.8	22.1	786431	4	US-09-751-389-3
24	35.2	21.7	658	3	US-08-998-416-595
25	35.2	21.7	5844	4	US-10-204-708-89
26	35.2	21.7	6182	4	US-10-204-708-88
C 27	35	21.6	855	4	US-08-961-527-245

C 28	35	21.6	1493	1	US-08-340-820-24	Sequence 24, Appl
C 29	35	21.6	1493	1	US-08-593-535-24	Sequence 24, Appl
C 30	35	21.6	3452	4	US-09-576-594-856	Sequence 856, App
C 31	35	21.6	11049	4	US-10-204-708-22	Sequence 22, Appl
C 32	35	21.6	13425	4	US-08-961-527-151	Sequence 151, App
C 33	35	21.6	1664976	4	US-08-916-421B-1	Sequence 1, Appli
34	34.8	21.5	783	4	US-08-956-171B-834	Sequence 834, App
C 35	34.8	21.5	6243	2	US-09-056-075-1	Sequence 1, Appli
36	34.6	21.4	19233	4	US-10-204-708-45	Sequence 45, Appl
37	34.4	21.2	1495	4	US-09-807-258-21	Sequence 21, Appl
38	34.4	21.2	6072	3	US-09-535-381-3	Sequence 3, Appli
39	34.2	21.1	1442	4	US-09-227-357-119	Sequence 119, App
40	34.2	21.1	5111	4	US-09-004-838-118	Sequence 118, App
41	34.2	21.1	6020	4	US-10-204-708-8	Sequence 8, Appli
42	34.2	21.1	19513	4	US-10-204-708-39	Sequence 39, Appl
C 43	34	21.0	732	4	US-09-134-000C-2779	Sequence 2779, Ap
C 44	34	21.0	1664976	4	US-08-916-421B-1	Sequence 1, Appli
C 45	33.8	20.9	998	3	US-09-122-400B-5	Sequence 5, Appli

ALIGNMENTS

RESULT 1

US-08-556-978B-78/c
; Sequence 78, Application US/08556978B
; Patent No. 6268169
; GENERAL INFORMATION:
; APPLICANT: FAHNESTOCK, STEPHEN F.
; TITLE OF INVENTION: NOVEL RECOMBINANTLY PRODUCED
; TITLE OF INVENTION: SPIDER SILK ANALOGS
; NUMBER OF SEQUENCES: 107
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: E. I. DU PONT DE NEMOURS AND COMPANY
; STREET: 1007 MARKET STREET
; CITY: WILMINGTON
; STATE: DELAWARE
; COUNTRY: UNITED STATES OF AMERICA
; ZIP: 19898
; COMPUTER READABLE FORM:
; MEDIUM TYPE: DISKETTE, 3.50 INCH
; COMPUTER: IBM PC COMPATIBLE
; OPERATING SYSTEM: MICROSOFT WINDOWS 95
; SOFTWARE: MICROSOFT WORD FOR WINDOWS 95
; CURRENT APPLICATION DATA: US/08/556,978B
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/077,600
; FILING DATE: JUNE 15, 1993
; ATTORNEY/AGENT INFORMATION:
; NAME: FLOYD, LINDA AXAMETHY
; REGISTRATION NUMBER: 33,692
; REFERENCE/DOCKET NUMBER: CR-9389-A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 302-892-8112
; TELEFAX: 302-773-0164
; INFORMATION FOR SEQ ID NO: 78:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4909 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: circular
; MOLECULE TYPE: DNA (genomic)
US-08-556-978B-78

Query March 99.0%; Score 160.4; DB 3; Length 4909;
Best Local Similarity 99.4%; Pred. No. 1.6e-26;
Matches 161; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 1 TCTGTTACAGTCTACTAATCCTACTAGTAGTTGATTGATGCTGCTATGTTGTG 60
|||||

Db 2516 TCTGTTACAGGTCACCTAATACCATCTAAGTAGTGTGATTCATAGTGAATGATGTTGTG 2457
QY 61 TTTTACAGTATTATAGTAGTCTGTTTTTATGCAAAATCTAAATTAATATATTGATATTTA 120
Db 2456 TTTTACAGTATTATAGTAGTCTGTTTTTATGCAAAATCTAAATTAATATATTGATATTTA 2397
QY 121 TATCATTTTACGTTTCTCGTTCAGCTTTTATATACAACTTG 162
Db 2396 TATCATTTTACGTTTCTCGTTCAGCTTTTATATACAACTTG 2355

RESULT 2

US-09-630-929-4/c
; Sequence 4, Application US/09630929
; Patent No. 6620585
; GENERAL INFORMATION:
; APPLICANT: Judith W. Zyskind
; TITLE OF INVENTION: USE OF ECOTOXINS AND SECRETED ENZYMES
; TITLE OF INVENTION: TO MONITOR CELLULAR PROLIFERATION
; FILE REFERENCE: ELITRA.012A
; CURRENT APPLICATION NUMBER: US/09/630,929
; CURRENT FILING DATE: 2000-08-02
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 6043
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Engineered E. coli plasmid pJFK4 with V. harveyi
; OTHER INFORMATION: sequences inserted
US-09-630-929-4

Query Match 99.0%; Score 160.4; DB 4; Length 6043;
Best Local Similarity 99.4%; Pred. No. 1.6e-28;
Matches 161; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TCTGTTACAGGTCACCTAATACCATCTAAGTAGTGTGATTCATAGTGAATGATGTTGTG 60
Db 5414 TCTGTTACAGGTCACCTAATACCATCTAAGTAGTGTGATTCATAGTGAATGATGTTGTG 5355
QY 61 TTTTACAGTATTATAGTAGTCTGTTTTTATGCAAAATCTAAATTAATATATTGATATTTA 120
Db 5354 TTTTACAGTATTATAGTAGTCTGTTTTTATGCAAAATCTAAATTAATATATTGATATTTA 5295
QY 121 TATCATTTTACGTTTCTCGTTCAGCTTTTATATACAACTTG 162
Db 5294 TATCATTTTACGTTTCTCGTTCAGCTTTTATATACAACTTG 5253

RESULT 3

US-07-590-988A-1
; Sequence 1, Application US/07590988A
; Patent No. 5227288
; GENERAL INFORMATION:
; APPLICANT: Blattner, Frederick R.
; TITLE OF INVENTION: DNA Sequencing Vector with
; TITLE OF INVENTION: Reversible Insert
; NUMBER OF SEQUENCES: 1
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Quarles and Brady
; STREET: P.O. BOX 2113
; STREET: FIRST WISCONSIN PLAZA
; CITY: MADISON
; STATE: WISCONSIN
; COUNTRY: U.S.A.
; ZIP: 53701
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette - 3.50 inch, 800Kb storage
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Macintosh
; SOFTWARE: Microsoft word 4.0
; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/07/590,988A
; FILING DATE: 19901001
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Nicholas J. Seay
; REGISTRATION NUMBER: 27,386
; REFERENCE/DOCKET NUMBER: 9629691682
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (608) 251-5000
; TELEFAX: (608) 251-9166
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7652 base pairs
; TYPE: NUCLEIC ACID
; STRANDEDNESS: double
; TOPOLOGY: circular
; MOLECULE TYPE: Other nucleic acid;
; DESCRIPTION: synthetic recombinant plasmid
; HYPOTHEICAL: no
; ANTI-SENSE: no
US-07-590-988A-1
Query Match 99.0%; Score 160.4; DB 1; Length 7652;
Best Local Similarity 99.4%; Pred. No. 1.6e-28;
Matches 161; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 TCTGTTACAGGTCACCTAATACCATCTAAGTAGTGTGATTCATAGTGAATGATGTTGTG 60
Db 5933 TCTGTTACAGGTCACCTAATACCATCTAAGTAGTGTGATTCATAGTGAATGATGTTGTG 5992
QY 61 TTTTACAGTATTATAGTAGTCTGTTTTTATGCAAAATCTAAATTAATATATTGATATTTA 120
Db 5993 TTTTACAGTATTATAGTAGTCTGTTTTTATGCAAAATCTAAATTAATATATTGATATTTA 6052
QY 121 TATCATTTTACGTTTCTCGTTCAGCTTTTATATACAACTTG 162
Db 6053 TATCATTTTACGTTTCTCGTTCAGCTTTTATATACAACTTG 6094
RESULT 4
US-09-453-702B-50
; Sequence 50, Application US/09453702B
; Patent No. 6365723
; GENERAL INFORMATION:
; APPLICANT: Blattner, Frederick R.
; Burland, Valerie
; Perna, Nicole T.
; Plunkett, Guy
; Welch, Rod
; TITLE OF INVENTION: No. 6365723el Sequences of E. coli O157
; NUMBER OF SEQUENCES: 285
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Quarles & Brady
; STREET: 1 South Pinckney Street
; CITY: Madison
; STATE: WI
; COUNTRY: US
; ZIP: 53701-2113
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.44Mb storage
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Word Perfect 8.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/453,702B
; FILING DATE: 03-Dec-1999
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/110,955
; FILING DATE: 04-DEC-1998
; ATTORNEY/AGENT INFORMATION:
; NAME: Seay, Nicholas J.
; REGISTRATION NUMBER: 27386

```

; REFERENCE/DOCKET NUMBER: 960296.95017
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (608) 251-5000
; TELEFAX: (608) 251-9166
; INFORMATION FOR SEQ ID NO: 50:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 38584
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; SEQUENCE DESCRIPTION: SEQ ID NO: 50:
US-09-453-702B-50

Query Match 64.6%; Score 104.6; DB 4; Length 38584;
Best Local Similarity 83.2%; Pred. No. 9.9e-16;
Matches 119; Conservative 0; Mismatches 24; Indels 0; Gaps 0;

QY 1 TCTGTTACAGGTCACCTAAATACCATCTAAGTAGTGTGATTCATAGTACTGATGCTGCATATGTTGTG 60
Db 38442 TCTGTTACAGGTCACCTAAATACCATCTAAGTAGTGTGATTCATAGTACTGATGCTGCATATGTTGTG 38501

QY 61 TTTTACAGTATTATGATGCTGTTTTTATGCAAAATCTAATTAAATATATTCATATTATTA 120
Db 38502 TTTTACAGTATTATGATGCTGTTTTTATGCAAAATCTAATTAAATATATTCATATTATTA 38561

QY 121 TATCATTTACGTTTCTCGTTCA 143
Db 38562 TGGGTTTTCGTTTCGCGTTCA 38584

RESULT 5
US-08-021-667A-17
; Sequence 17, Application US/08021667A
; Patent No. 5434049
; GENERAL INFORMATION:
; APPLICANT: Okano, Kazunori
; APPLICANT: Kambara, Hideki
; TITLE OF INVENTION: POLYNUCLEOTIDE CAPTURING TIP AND
; TITLE OF INVENTION: POLYNUCLEOTIDE PREPARATIVE METHOD AND DETECTION
; TITLE OF INVENTION: METHOD USING SAME
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Antonelli, Terry, Stout & Kraus
; STREET: Suite 600, 1919 Pennsylvania Ave., NW
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20006
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/021.667A
; FILING DATE: 19930224
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Terry, David T.
; REGISTRATION NUMBER: 20,178
; REFERENCE/DOCKET NUMBER: 520.31930X00
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-828-0380
; TELEFAX: 202-828-0380
; TELEX: 440280/248545
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 200 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: YES
; ANTI-SENSE: NO
US-08-410-544-17

Query Match 60.1%; Score 97.4; DB 1; Length 200;
Best Local Similarity 99.0%; Pred. No. 3.1e-14;
Matches 98; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TCTGTTACAGGTCACCTAAATACCATCTAAGTAGTGTGATTCATAGTACTGATGCTGCATATGTTGTG 60
Db 102 TCTGTTACAGGTCACCTAAATACCATCTAAGTAGTGTGATTCATAGTACTGATGCTGCATATGTTGTG 161

QY 61 TTTTACAGTATTATGATGCTGTTTTTATGCAAAATCT 99
Db 162 TTTTACAGTATTATGATGCTGTTTTTATGCAAAATCT 200
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; HYPOTHETICAL: YES
; ANTI-SENSE: NO
US-08-021-667A-17

Query Match 60.1%; Score 97.4; DB 1; Length 200;
Best Local Similarity 99.0%; Pred. No. 3.1e-14;
Matches 98; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TCTGTTACAGGTCACCTAAATACCATCTAAGTAGTGTGATTCATAGTACTGATGCTGCATATGTTGTG 60
Db 102 TCTGTTACAGGTCACCTAAATACCATCTAAGTAGTGTGATTCATAGTACTGATGCTGCATATGTTGTG 161

QY 61 TTTTACAGTATTATGATGCTGTTTTTATGCAAAATCT 99
Db 162 TTTTACAGTATTATGATGCTGTTTTTATGCAAAATCT 200

RESULT 6
US-08-410-544-17
; Sequence 17, Application US/08410544
; Patent No. 5607646
; GENERAL INFORMATION:
; APPLICANT: Okano, Kazunori
; APPLICANT: Kambara, Hideki
; TITLE OF INVENTION: POLYNUCLEOTIDE CAPTURING TIP AND
; TITLE OF INVENTION: POLYNUCLEOTIDE PREPARATIVE METHOD AND DETECTION
; TITLE OF INVENTION: METHOD USING SAME
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Antonelli, Terry, Stout & Kraus
; STREET: Suite 600, 1919 Pennsylvania Ave., NW
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20006
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/410,544
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/021,667
; FILING DATE: 24-FEB-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Terry, David T.
; REGISTRATION NUMBER: 20,178
; REFERENCE/DOCKET NUMBER: 520.31930X00
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-828-0300
; TELEFAX: 202-828-0380
; TELEX: 248545
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 200 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: YES
; ANTI-SENSE: NO
US-08-410-544-17

Query Match 60.1%; Score 97.4; DB 1; Length 200;
Best Local Similarity 99.0%; Pred. No. 3.1e-14;
Matches 98; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TCTGTTACAGGTCACCTAAATACCATCTAAGTAGTGTGATTCATAGTACTGATGCTGCATATGTTGTG 60
Db 102 TCTGTTACAGGTCACCTAAATACCATCTAAGTAGTGTGATTCATAGTACTGATGCTGCATATGTTGTG 161
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QY 61 TTTTACAGTATTAGTCTAGTCTGTTTTTTTATGCAAAATCT 99
Db 162 TTTTACAGTATTAGTCTAGTCTGTTTTTTTATGCAAAATCT 200

RESULT 7
US-08-728-785A-17
; Sequence 17, Application US/08728785A
; Patent No. 5817506
; GENERAL INFORMATION:
; APPLICANT: Okano, Kazunori
; APPLICANT: Kambara, Hideki
; TITLE OF INVENTION: POLYNUCLEOTIDE CAPTURING TIP AND
; TITLE OF INVENTION: POLYNUCLEOTIDE PREPARATIVE METHOD AND DETECTION
; TITLE OF INVENTION: METHOD USING SAME
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Antorelli, Terry, Stout & Kraus
; STREET: Suite 1800, 1300 No. 5817506th Seventeenth St.
; CITY: Arlington
; STATE: VA
; COUNTRY: USA
; ZIP: 22209
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/728,785A
; FILING DATE: 10-OCT-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/410,544
; FILING DATE: 21-MAR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/021,667
; FILING DATE: 24-FEB-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Terry, David T.
; REGISTRATION NUMBER: 20,178
; REFERENCE/DOCKET NUMBER: 520.31930X00
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-312-6600
; TELEFAX: 703-312-6666
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 200 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHEICAL: YES
; ANTI-SENSE: NO
; US-08-728-785A-17

Query Match 60.1%; Score 97.4; DB 1; Length 200;
Best Local Similarity 99.0%; Pred. No. 3.1e-14;
Matches 98; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TCTGTTACAGTCACTAATACCATCTAGTCTGTTGATTCATAGTGCATATGTTGTG 60
Db 102 TCTGTTACAGTCACTAATACCATCTAGTCTGTTGATTCATAGTGCATATGTTGTG 161

QY 61 TTTTACAGTATTAGTCTGTTTTTTTATGCAAAATCT 99
Db 162 TTTTACAGTATTAGTCTGTTTTTTTATGCAAAATCT 200

RESULT 8
US-09-453-702B-66/c
; Sequence 66, Application US/09453702B
```

```
; Patent No. 6365723
; GENERAL INFORMATION:
; APPLICANT: Blattner, Frederick R.
; APPLICANT: Burland, Valerie
; APPLICANT: Perna, Nicole T.
; APPLICANT: Plunkett, Guy
; APPLICANT: Welch, Rod
; TITLE OF INVENTION: No. 6365723el Sequences of E. coli O157
; NUMBER OF SEQUENCES: 265
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Quarles & Brady
; STREET: 1 South Pinckney Street
; CITY: Madison
; STATE: WI
; COUNTRY: US
; ZIP: 53701-2113
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.44Mb storage
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Word Perfect 8.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/453,702B
; FILING DATE: 03-Dec-1999
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/110,955
; FILING DATE: 04-DEC-1998
; ATTORNEY/AGENT INFORMATION:
; NAME: Seay, Nicholas J.
; REGISTRATION NUMBER: 27386
; REFERENCE/DOCKET NUMBER: 960296.95017
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (608) 251-5000
; TELEFAX: (608) 251-9166
; INFORMATION FOR SEQ ID NO: 66:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9827
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; SEQUENCE DESCRIPTION: SEQ ID NO: 66:
US-09-453-702B-66

Query Match 41.9%; Score 67.8; DB 4; Length 9827;
Best Local Similarity 69.0%; Pred. No. 2.3e-07;
Matches 107; Conservative 0; Mismatches 47; Indels 1; Gaps 1;

QY 1 TCTGTTACAGTCACTAATACCATCTAGTCTGTTGATTCATAGTGCATATGTTGT- 59
Db 938 TCTGAACAGGTCACTAATATCATCTAAATAGTTGACTCATAGTGACAGCATGTTGTG 879

QY 60 GTTTTACAGTATTAGTCTGTTTTTTTATGCAAAATCTAATTAAATATGATATT 119
Db 878 GTCTTGAGTATTATATAGCCTATTATTGATTCAGCCATCATATCTATTGATCGT 819

QY 120 ATATCATTTTACGTTTCTCGTTTCAGCTTTTATA 154
Db 818 AAATGGGTTTTTATTGTTGGTGGTGGCGCTTTTAA 784

RESULT 9
US-08-021-667A-18
; Sequence 18, Application US/08021667A
; Patent No. 5434049
; GENERAL INFORMATION:
; APPLICANT: Okano, Kazunori
; APPLICANT: Kambara, Hideki
; TITLE OF INVENTION: POLYNUCLEOTIDE CAPTURING TIP AND
; TITLE OF INVENTION: POLYNUCLEOTIDE PREPARATIVE METHOD AND DETECTION
; TITLE OF INVENTION: METHOD USING SAME
; NUMBER OF SEQUENCES: 18
```


; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Antonelli, Terry, Stout & Kraus
 ; STREET: Suite 600, 1919 Pennsylvania Ave., NW
 ; CITY: Washington
 ; STATE: DC
 ; COUNTRY: USA
 ; ZIP: 20006
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent In Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/021,667A
 ; FILING DATE: 19930224
 ; CLASSIFICATION: 435
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Terry, David T.
 ; REGISTRATION NUMBER: 20,178
 ; REFERENCE/DOCKET NUMBER: 520.31930X00
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 202-828-0300
 ; TELEFAX: 202-828-0380
 ; TELEX: 440280/248545
 ; INFORMATION FOR SEQ ID NO: 18:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 201 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: DNA (genomic)
 ; HYPOTHETICAL: YES
 ; ANTI-SENSE: NO
 ; US-08-021-667A-18

Query Match 37.9%; Score 61.4; DB 1; Length 201;
 Best Local Similarity 98.4%; Pred. No. 5.1e-06;
 Matches 62; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 100 AATTATATATGATATTTATATCATTTTACGTTCTCGTTACGCTTTTATACCTAAAC 159
 Db 1 AATTATATATGATATTTATATCATTTTACGTTCTCGTTACGCTTTTATACCTAAAG 60
 QY 160 TTG 162
 Db 61 TTG 63

RESULT 10
 US-08-410-544-18
 ; Sequence 18, Application US/08410544
 ; Patent No. 5607646
 ; GENERAL INFORMATION:
 ; APPLICANT: Okano, Kazunori
 ; TITLE OF INVENTION: POLYNUCLEOTIDE CAPTURING TIP AND
 ; TITLE OF INVENTION: POLYNUCLEOTIDE PREPARATIVE METHOD AND DETECTION
 ; TITLE OF INVENTION: METHOD USING SAME
 ; NUMBER OF SEQUENCES: 18
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Antonelli, Terry, Stout & Kraus
 ; STREET: Suite 600, 1919 Pennsylvania Ave., NW
 ; CITY: Washington
 ; STATE: DC
 ; COUNTRY: USA
 ; ZIP: 20006
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent In Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/410,544

; FILING DATE:
 ; CLASSIFICATION: 435
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 08/021,667
 ; FILING DATE: 24-FEB-1993
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Terry, David T.
 ; REGISTRATION NUMBER: 20,178
 ; REFERENCE/DOCKET NUMBER: 520.31930X00
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 202-828-0300
 ; TELEFAX: 202-828-0380
 ; TELEX: 248545
 ; INFORMATION FOR SEQ ID NO: 18:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 201 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: DNA (genomic)
 ; HYPOTHETICAL: YES
 ; ANTI-SENSE: NO
 ; US-08-410-544-18

Query Match 37.9%; Score 61.4; DB 1; Length 201;
 Best Local Similarity 98.4%; Pred. No. 5.1e-06;
 Matches 62; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 100 AATTATATATGATATTTATATCATTTTACGTTCTCGTTACGCTTTTATACCTAAAC 159
 Db 1 AATTATATATGATATTTATATCATTTTACGTTCTCGTTACGCTTTTATACCTAAAG 60
 QY 160 TTG 162
 Db 61 TTG 63

RESULT 11
 US-08-728-785A-18
 ; Sequence 18, Application US/08728785A
 ; Patent No. 5817506
 ; GENERAL INFORMATION:
 ; APPLICANT: Okano, Kazunori
 ; APPLICANT: Kambara, Hideki
 ; TITLE OF INVENTION: POLYNUCLEOTIDE CAPTURING TIP AND
 ; TITLE OF INVENTION: POLYNUCLEOTIDE PREPARATIVE METHOD AND DETECTION
 ; TITLE OF INVENTION: METHOD USING SAME
 ; NUMBER OF SEQUENCES: 18
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Antonelli, Terry, Stout & Kraus
 ; STREET: Suite 1800, 1300 No. 5817506th Seventeenth St.
 ; CITY: Arlington
 ; STATE: VA
 ; COUNTRY: USA
 ; ZIP: 22209
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent In Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/728,785A
 ; FILING DATE: 10-OCT-1996
 ; CLASSIFICATION: 435
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 08/410,544
 ; FILING DATE: 21-MAR-1995
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 08/021,667
 ; FILING DATE: 24-FEB-1993
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Terry, David T.
 ; REGISTRATION NUMBER: 20,178

RESULT 13
US-08-487-826B-13/c
; Sequence 13, Application US/08487826B
; Patent No. 5993827
; GENERAL INFORMATION:

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RESULT 14
US-09-790-988-1/c
; Sequence 1, Application US/09790986
; Patent No. 6632935
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; GENERAL INFORMATION:
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; APPLICANT: SHIGENOBU, SHUJI
; APPLICANT: WATANABE, HIDEMI
; APPLICANT: HATTORI, MASAHIRA
; APPLICANT: SAKAKI, YOSHIYUKI
;
; TITLE OF INVENTION: GENOME DNA OF H
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; FILE REFERENCE: 081356/0159
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; CURRENT APPLICATION NUMBER: US/09/
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; CURRENT FILING DATE: 2001-02-23
;

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Fri Sep 10 09:49:26 2004

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; PRIOR APPLICATION NUMBER: JP2000-107160
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 640681
; TYPE: DNA
; ORGANISM: Buchnera sp.
US-09-790-988-1

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Best Local Similarity 54.3%; Pred. No. 2.3; Indels 0; Gaps 0;
Matches 76; Conservative 0; Mismatches 64;

QY 12 TCACTAATACCATCTAAGTAGTGTGATTCATAGTAGTGCATATGTTGTGTTTACAGTAT 71
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Db 451255 ATTATATTTTAAATTAATAATAAATTAATTAATATATATATATATGATCTAATATTAGTAAT 451196
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RESULT 15
US-09-790-988-2
; Sequence 2, Application US/09790988
; Patent No. 6632935
; GENERAL INFORMATION:
; APPLICANT: SHIGENOBU, SHUJI
; APPLICANT: WATANABE, HIDEMI
; APPLICANT: HATTORI, MASAHIRA
; APPLICANT: SAKAKI, YOSHIYUKI
; TITLE OF INVENTION: GENOME DNA OF BACTERIAL SYMBIONT OF APHIDS
; FILE REFERENCE: 081356/0159
; CURRENT APPLICATION NUMBER: US/09/790,988
; CURRENT FILING DATE: 2001-02-23
; PRIOR APPLICATION NUMBER: JP2000-107160
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn Ver. 2.1
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; ORGANISM: Buchnera sp.
US-09-790-988-2

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Best Local Similarity 57.1%; Pred. No. 1.9; Indels 0; Gaps 0;
Matches 68; Conservative 0; Mismatches 51;

QY 42 AGTGACATGATATCTGTTGTTTACAGTATATATAGTCTGTTTATGCAAAATCTAA 101
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QY 102 TTTAATATATGATATTTATATCACTTTTACGTTTCTCGTCTGTTTATCTAACT 160
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Search completed: September 9, 2004, 21:21:23
Job time : 39.7198 secs
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: September 9, 2004, 17:30:16 ; Search time 1308.61 Seconds
(without alignments)
3696.811 Million cell updates/sec

Title: US-10-082-772B-4

Perfect score: 162

Sequence: 1 tctgtacaggtcactaata.....agcttttttatactaacttg 162

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 27513289 seqs, 14931090276 residues

Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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9: gb_est1:*
10: gb_est2:*
11: gb_hic:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
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16: em_estom:*
17: em_gss_hum:*
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29: gb_gss2:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	162	100.0	770	28	AQ991774
C 2	162	100.0	791	28	AQ991791
C 3	160.4	99.0	712	28	AQ990809
C 4	155.4	95.9	708	28	AQ990869

5	154	95.1	299	13	BY115594
6	150.6	93.0	827	14	CF347641
7	149.6	92.3	787	14	CF347604
8	149	92.0	755	14	CF347718
C 9	140.8	86.9	756	28	AQ991732
C 10	137.8	85.1	777	14	CF347686
C 11	134.5	83.1	583	14	CB403882
C 12	133.8	82.6	395	28	AQ991303
C 13	129.8	80.1	393	14	CB403984
C 14	128.8	79.5	769	28	AQ990470
C 15	126.2	77.9	764	28	AQ990878
C 16	123.6	76.3	487	14	CB395230
C 17	121	74.7	556	28	AQ991338
C 18	114.8	70.9	743	28	AQ990346
C 19	114.4	70.6	472	13	BQ157398
C 20	114.4	70.6	473	13	BQ156404
C 21	114.2	70.5	758	28	AQ991690
C 22	104.8	64.7	751	28	AQ989566
C 23	103	63.5	753	28	AQ990861
C 24	102.8	63.5	553	14	CF347596
C 25	94.2	58.1	746	28	AQ990173
C 26	92.2	56.9	811	14	CF347776
C 27	88.8	54.8	808	28	AQ990388
C 28	88.8	54.8	810	14	CF347481
C 29	86.8	53.6	719	28	AQ991352
C 30	81.6	50.4	715	28	AQ991358
C 31	76.8	47.4	695	28	AQ991039
C 32	76.2	47.0	384	12	B1174407
C 33	74.6	46.0	767	28	AQ990301
C 34	67.4	41.6	597	12	B1422679
C 35	67.2	41.5	800	14	CF347726
C 36	62.8	38.8	764	28	AQ990110
C 37	61.4	37.9	206	13	BQ156416
C 38	57.8	35.7	767	14	CF347722
C 39	54.8	33.8	329	9	AA386440
C 40	54.8	33.8	823	14	CF347730
C 41	50.6	31.2	675	28	AQ991241
C 42	47	29.0	609	28	AZ522574
C 43	46.8	28.9	692	28	AQ990864
C 44	46.4	28.6	591	14	CB404318
C 45	46.4	28.6	737	29	BX154196

ALIGNMENTS

RESULT 1
AQ991774/c

LOCUS

DEFINITION

AQ991774 770 bp DNA linear GSS 14-AUG-2000
Rfc02039F Photorhabdus luminescens strain W14 M13 library
Photorhabdus luminescens genomic clone PLG02039F, genomic survey
sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

MEDLINE

PUBMED

COMMENT

AQ991774.1 GI:9650368

GSS.

Photorhabdus luminescens

Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;

Enterobacteriaceae; Photorhabdus.

1 (bases 1 to 770)

ffrench-Constant, R.H., Waterfield, N., Burland, V., Perna, N.T.,

Daborn, P.J., Bowen, D. and Blattner, F.R.

A genomic sample sequence of the entomopathogenic bacterium

Photorhabdus luminescens W14: potential implications for virulence

Appl. Environ. Microbiol. 66 (8), 3310-3329 (2000)

20378633

10919786

Contact: ffrench-Constant RH

Department of Biology and Biochemistry

University of Bath

South Building, Bath BA2 7AY, UK

Tel: (44) 1225 826621

Fax: (44) 1225 826779

Email: bssrfc@bath.ac.uk
 This is one of a selected subset of flipped clones from the M13 library. For annotation of identified clones (BLASTX, BLASTN and mapping to E. coli K12 genome) please see ffrench-Constant et al. 2000, Nucleic Acids Res.
 Seq primer: M13 Reverse
 Class: shotgun.

FEATURES

source
 1. .770
 /organism="Photorhabdus luminescens"
 /mol_type="genomic DNA"
 /strain="W14"
 /db_xref="taxon:29488"
 /clone="PLG02039F"
 /dev_stage="primary phase variant"
 /clone_lib="Photorhabdus luminescens strain W14 M13 library"
 /note="Genomic DNA from strain W14 was size selected (1-2 kb) and then cloned into M13 Janus."

ORIGIN

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 Best Local Similarity 100.0%; Pred. No. 7.3e-22;
 Matches 162; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 TCTGTTACAGGTCACCTAATACCATCTAAGTAGTTCATTCATAGTGCATATGTTGTG 60
 Db 197 TCTGTTACAGGTCACCTAATACCATCTAAGTAGTTCATTCATAGTGCATATGTTGTG 138
 QY 61 TTTTACAGTATTATGATGCTCTGTTTTTATGCAAAATCTAATTTAATATATTGATATTTA 120
 Db 137 TTTTACAGTATTATGATGCTCTGTTTTTATGCAAAATCTAATTTAATATATTGATATTTA 78
 QY 121 TATCATTTTACGTTTCTGTTTCAGCTTTTATGCAAAATCTAATTTAATATATTGATATTTA 162
 Db 77 TATCATTTTACGTTTCTGTTTCAGCTTTTATGCAAAATCTAATTTAATATATTGATATTTA 36

RESULT 2

AQ991791/c
 LOCUS 791 bp DNA linear GSS 14-AUG-2000
 DEFINITION Rf02368F Photorhabdus luminescens strain W14 M13 library
 Photorhabdus luminescens genomic clone PLG02368F, genomic survey sequence.
 ACCESSION AQ991791.1 GI:9650385
 VERSION AQ991791.1
 KEYWORDS GSS.
 SOURCE Photorhabdus luminescens
 ORGANISM Photorhabdus luminescens
 Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales; Enterobacteriaceae; Photorhabdus.
 REFERENCE 1 (bases 1 to 791)
 AUTHORS ffrench-Constant,R.H., Waterfield,N., Burland,V., Perna,N.T., Daborn,P.J., Bowen,D. and Blattner,F.R.
 TITLE A genomic sample sequence of the entomopathogenic bacterium Photorhabdus luminescens W14: potential implications for virulence
 JOURNAL Appl. Environ. Microbiol. 66 (8), 3310-3329 (2000)
 MEDLINE 20378633
 PUBMED 10919786
 COMMENT Contact: ffrench-Constant RH
 Department of Biology and Biochemistry
 University of Bath
 South Building, Bath BA2 7AY, UK
 Tel: (44) 1225 826621
 Fax: (44) 1225 826779
 Email: bssrfc@bath.ac.uk

This is one of a selected subset of flipped clones from the M13 library. For annotation of identified clones (BLASTX, BLASTN and mapping to E. coli K12 genome) please see ffrench-Constant et al. 2000, Nucleic Acids Res.
 Seq primer: M13 Reverse
 Class: shotgun.

FEATURES

Location/Qualifiers

source

1. .791
 /organism="Photorhabdus luminescens"
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 /strain="W14"
 /db_xref="taxon:29488"
 /clone="PLG02368F"
 /dev_stage="primary phase variant"
 /clone_lib="Photorhabdus luminescens strain W14 M13 library"
 /note="Genomic DNA from strain W14 was size selected (1-2 kb) and then cloned into M13 Janus."

ORIGIN

Query Match 100.0%; Score 162; DB 28; Length 791;
 Best Local Similarity 100.0%; Pred. No. 7.2e-22;
 Matches 162; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 TCTGTTACAGGTCACCTAATACCATCTAAGTAGTTCATTCATAGTGCATATGTTGTG 60
 Db 194 TCTGTTACAGGTCACCTAATACCATCTAAGTAGTTCATTCATAGTGCATATGTTGTG 135
 QY 61 TTTTACAGTATTATGATGCTCTGTTTTTATGCAAAATCTAATTTAATATATTGATATTTA 120
 Db 134 TTTTACAGTATTATGATGCTCTGTTTTTATGCAAAATCTAATTTAATATATTGATATTTA 75
 QY 121 TATCATTTTACGTTTCTGTTTCAGCTTTTATGCAAAATCTAATTTAATATATTGATATTTA 162
 Db 74 TATCATTTTACGTTTCTGTTTCAGCTTTTATGCAAAATCTAATTTAATATATTGATATTTA 33

RESULT 3

AQ990809/c
 LOCUS 712 bp DNA linear GSS 14-AUG-2000
 DEFINITION Rf01638 Photorhabdus luminescens strain W14 M13 library
 Photorhabdus luminescens genomic clone PLG01638, genomic survey sequence.
 ACCESSION AQ990809.1 GI:9649403
 VERSION AQ990809.1
 KEYWORDS GSS.
 SOURCE Photorhabdus luminescens
 ORGANISM Photorhabdus luminescens
 Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales; Enterobacteriaceae; Photorhabdus.
 REFERENCE 1 (bases 1 to 712)
 AUTHORS ffrench-Constant,R.H., Waterfield,N., Burland,V., Perna,N.T., Daborn,P.J., Bowen,D. and Blattner,F.R.
 TITLE A genomic sample sequence of the entomopathogenic bacterium Photorhabdus luminescens W14: potential implications for virulence
 JOURNAL Appl. Environ. Microbiol. 66 (8), 3310-3329 (2000)
 MEDLINE 20378633
 PUBMED 10919786
 COMMENT Contact: ffrench-Constant RH
 Department of Biology and Biochemistry
 University of Bath
 South Building, Bath BA2 7AY, UK
 Tel: (44) 1225 826621
 Fax: (44) 1225 826779
 Email: bssrfc@bath.ac.uk

This is one of 2,122 random reads from the M13 library. For annotation of identified clones (BLASTX, BLASTN and mapping to E. coli K12 genome) please see ffrench-Constant et al. 2000, Nucleic Acids Res
 Seq primer: M13 Forward
 Class: shotgun.

FEATURES

Location/Qualifiers
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 /mol_type="genomic DNA"
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/notes="Genomic DNA from strain W14 was size selected (1-2
kb) and then cloned into M13 Janus."

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Best Local Similarity 99.4%; Pred. No. 1.5e-21;
Matches 161; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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QY 61 TTTTACAGTATTATGAGTCTGTTTTTATGCGAAAATCTAATTATATATATGATATTA 120
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Db 531 TTTTACAGTATTATGAGTCTGTTTTTATGCGAAAATCTAATTATATATATGATATTA 472

QY 121 TATCATTTTACGTTTCTCGTTTCAGCTTTTATATACAACTTG 162
    |||||
Db 471 TATCATTTTACGTTTCTCGTTTCAGCTTTTATATACAACTTG 430

RESULT 4
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LOCUS
DEFINITION
Rfco1706 Photorhabdus luminescens strain W14 M13 library
Photorhabdus luminescens genomic clone PLG01706, genomic survey
sequence.
ACCESSION
AQ990869
VERSION
AQ990869.1 GI:9649463
KEYWORDS
GSS.
SOURCE
Photorhabdus luminescens
ORGANISM
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Photorhabdus.
REFERENCE
1 (bases 1 to 708)
french-Constant,R.H., Waterfield,N., Burland,V., Perna,N.T.,
Daborn,P.J., Bowen,D. and Blattner,F.R.
A genomic sample sequence of the entomopathogenic bacterium
Photorhabdus luminescens W14: potential implications for virulence
Appl. Environ. Microbiol. 66 (8), 3310-3329 (2000)
20378633
JOURNAL
Microbiol.
MEDLINE
10919786
PUBMED
Contact: french-Constant RH
Department of Biology and Biochemistry
University of Bath
South Building, Bath BA2 7AY, UK
Tel: (44) 1225 826621
Fax: (44) 1225 826779
Email: bsr@c Bath.ac.uk
This is one of 2,122 random reads from the M13 library. For
annotation of identified clones (BLASTX, BLASTN and mapping to E.
coli K12 genome) please see french-Constant et al. 2000, Nucleic
Acids Res.
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Best Local Similarity 99.4%; Pred. No. 1.4e-20;
Matches 156; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Db 421 CAGTATTATGAGTCTGTTTATGCGAAAATCTAATTATATATGATATATATATCA 362

QY 126 TTTTACGTTTCTCGTTTCAGCTTTTATATACAACTTG 162
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Db 361 TTTTACGTTTCTCGTTTCAGCTTTTATATACAACTTG 325

RESULT 5
BY115594
LOCUS
DEFINITION
BY115594 RIKEN full-length enriched, 18 days embryo whole body Mus
musculus cDNA clone L430040C03 5', mRNA sequence.
ACCESSION
BY115594
VERSION
BY115594.1 GI:26226695
KEYWORDS
EST.
SOURCE
Mus musculus (house mouse)
ORGANISM
Mus musculus
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
1 (bases 1 to 299)
Okazaki,Y., Furuno,M., Kasukawa,T., Adachi,J., Bono,H., Kondo,S.,
Nikaido,I., Osato,N., Saito,R., Suzuki,H., Yamanaoka,I.,
Kiyosawa,H., Yagi,K., Tomaru,Y., Hasegawa,Y., Nogami,A.,
Schonbach,C., Gojobori,T., Baldarelli,R., Hill,D.P., Bult,C.,
Hume,D.A., Quackenbush,J., Schriml,L.M., Kanapin,A., Matsuda,H.,
Batalov,S., Beisel,K.W., Blake,J.A., Bradt,D., Bruscia,V.,
Ciothia,C., Corbani,L.E., Cousins,S., Dalla,E., Dragani,T.A.,
Fletcher,C.F., Forrest,A., Frazer,K.S., Gaasterland,T.,
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Gustinch,S., Hirokawa,N., Jackson,I.J., Jarvis,E.D., Kanai,A.,
Kawaji,H., Kawasawa,Y., Kedzierski,R.M., King,B.L., Konagaya,A.,
Kurochkin,I.V., Lee,Y., Lenhard,B., Lyons,P.A., Maglott,D.R.,
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Numata,K., Okido,T., Pavan,W.J., Pertea,G., Pesole,G.,
Petrovsky,N., Pillai,R., Pontius,J.U., Qi,D., Ramchandran,S.,
Ravasi,T., Reed,J.C., Reed,D.J., Reid,J., Ring,B.Z., Ringwald,M.,
Sandelin,A., Schneider,C., Sempie,C.A., Setou,M., Shimada,K.,
Sultana,R., Takenaka,Y., Taylor,M.S., Teasdale,R.D., Tomita,M.,
Wells,C., Wilming,I.G., Wynshaw-Boris,A., Yanagisawa,M., Yang,I.,
Yang,L., Yuan,Z., Zavolan,M., Zhu,Y., Zimmer,A., Carninci,P.,
Hayatsu,N., Hirozane-Kishikawa,T., Konno,H., Nakamura,M.,
Sakazume,N., Sato,K., Shiraki,T., Waki,K., Kawai,J., Aizawa,K.,
Arakawa,T., Fukuda,S., Hara,A., Hashizume,W., Imotani,K., Ishii,Y.,
Itoh,M., Kagawa,I., Miyazaki,A., Sakai,K., Sasaki,D., Shibata,K.,
Shinagawa,A., Yasunishi,A., Yoshino,M., Waterston,R., Lander,E.S.,
Rogers,J., Birney,E. and Hayashizaki,Y.
Analysis of the mouse transcriptome based on functional annotation
of 60,770 full-length cDNAs
Nature 420, 563-573 (2002)
12466851
JOURNAL
MEDLINE
22354683
PUBMED
Contact: Yoshihide Hayashizaki
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Sciences Center (GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-Ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-9222
Fax: 81-45-503-9216
Email: genome-res@sc.riken.go.jp,
URL:http://genome.gsc.riken.go.jp/
Aizawa,K., Akimura,T., Arakawa,T., Carninci,P., Fukuda,S.,
Hirozane,T., Imotani,K., Ishii,Y., Itoh,M., Kawai,J., Konno,H.,
Miyazaki,A., Murata,M., Nakamura,M., Nomura,K., Numazaki,R.,
Ohno,M., Sakai,K., Sakazume,N., Sasaki,D., Sato,K., Shibata,K.,
Shiraki,T., Tagami,M., Waki,K., Watanabe,A., Muramatsu,M. and

```

Havashizaki, Y. Direct Submission
Computational Analysis of Full-Length Mouse cDNAs Compared with Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)
Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000)
RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000)
Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a non-redundant cDNA library. Genome Res. 11 (2), 281-289 (2001)
cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.
Please visit our web site (<http://genome.gsc.riken.go.jp>) for further details.

FEATURES

Location/Qualifiers
1..239
/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="L430040C03"
/tissue_type="whole body"
/dev_stage="18 days embryo"
/clone_lib="RIKEN full-length enriched, 18 days embryo whole body"

ORIGIN

Query Match 95.1%; Score 154; DB 13; Length 299;
Best Local Similarity 96.9%; Pred. No. 3.4e-20;
Matches 157; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 TCTGTTACAGGTCACATATACCATCTAAGTAGTTGATTCATAGTGACATGCTATGTTGG 60
DB 108 TCTGTCACAGGTCACATATACCATCTAAGTAGTTGATTCATAGTGACATGCTATGTTGG 167

QY 61 TTTTACAGTATTATGATGATGCTCTGTTTTTATGCAAAATCTAATTTAATATATTGATTTTA 120
DB 168 TTTTACAGTATTATGATGATGCTCTGTTTTTATGCAAAATCTAATTTAATATATTGATTTTA 227

QY 121 TATCATTTTACGTTTCTCGTTTCAGCTTTTATATCACTTGG 162
DB 228 TATCATTTTACGTTTCTCGTTTCAGCTTTTATATCACTTGG 269

RESULT 6
CF347641
LOCUS
DEFINITION AGNCOURT_15225345 NIH_ZGC_10 Danio rerio cDNA clone IMAGE:7001697
5', mRNA sequence.
ACCESSION CF347641
VERSION CF347641.1 GI:33790724
KEYWORDS EST.
SOURCE Danio rerio (zebrafish)
ORGANISM Danio rerio
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes; Cyprinidae; Danio.
REFERENCE 1 (bases 1 to 827)
AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Daniela S. Gerhard, Ph.D.
Office of Cancer Genomics
National Cancer Institute / NIH
Bldg. 31 Rm10A07 Bethesda, MD 20892
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Len Zon, Harvard
cDNA Library Preparation: Open Biosystems

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
Plate: LLAM14695 row: g column: 08
High quality sequence start: 26
High quality sequence stop: 468.
Location/Qualifiers
1..827

FEATURES

Location/Qualifiers
1..827
/organism="Danio rerio"
/mol_type="mRNA"
/db_xref="taxon:7955"
/clone="IMAGE:7001697"
/tissue_type="whole body"
/lab_host="DH10B"
/clone_lib="NIH_ZGC_10"
/note="Vector: pEXpress1; Site 1: NotI; Site 2: EcoRV;
Bulk tissue was collected from a whole adult individual from the Tuebingen strain. 1st strand cDNA was primed with a Not I - oligo(dT) primer, double-stranded cDNA was cloned into the Not I and EcoRV sites of pEXpress-1. Library was size-selected for >1 kb fragments. A normalized version of this library is also available (NIH_ZGC_7). Library was constructed by Open Biosystems (Huntsville, AL)."

ORIGIN

Query Match 93.0%; Score 150.6; DB 14; Length 827;
Best Local Similarity 97.5%; Pred. No. 1.1e-19;
Matches 153; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 6 TACAGGTCACTAATACCATCTAAGTAGTTGATTCATAGTGACATGCTATGTTGTTTAA 65
DB 88 TACAGGTCACTAATACCATCTAAGTAGTTGTTTCATAGTGACATGCTATGTTGTTTAA 147

QY 66 CAGTATTATGATGCTGTTTTTATGCAAAATCTAATTTAATATATTGATTTATATCA 125
DB 148 CAGTATTATGATGCTGTTTTTATGCAAAATCTAATTTAATATATTGATTTATATCA 207

QY 126 TTTTACGTTTCTCGTTTCAGCTTTTATATCACTTGG 162
DB 208 TTTTACGTTTCTCGTTTCAGCTTTTATATCACTTGG 244

RESULT 7
CF347604
LOCUS
DEFINITION AGNCOURT_15225252 NIH_ZGC_10 Danio rerio cDNA clone IMAGE:7001739
5', mRNA sequence.
ACCESSION CF347604
VERSION CF347604.1 GI:33790651
KEYWORDS EST.
SOURCE Danio rerio (zebrafish)
ORGANISM Danio rerio
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes; Cyprinidae; Danio.
REFERENCE 1 (bases 1 to 787)
AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Daniela S. Gerhard, Ph.D.
Office of Cancer Genomics
National Cancer Institute / NIH
Bldg. 31 Rm10A07 Bethesda, MD 20892
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Len Zon, Harvard
cDNA Library Preparation: Open Biosystems
DNA Sequencing by: The I.M.A.G.E. Consortium (LLNL)
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov
 Plate: LLAM14695 row: i column: 02
 High quality sequence stop: 698.
 Location/Qualifiers

FEATURES

source

1. .787
 /organism="Danio rerio"
 /mol_type="mRNA"
 /db_xref="taxon:7955"
 /clone="IMAGE:7001739"
 /tissue_type="whole body"
 /lab_host="DH10B"
 /clone_lib="NIH_ZGC_10"
 /notes="Vector: pExpress1; Site 1: NotI; Site 2: EcoRV;
 Bulk tissue was collected from a whole adult individual
 from the Tuebingen strain. 1st strand cDNA was primed with
 a Not I - oligo(dT) primer, double-stranded cDNA was
 cloned into the Not I and EcoRV sites of pExpress-1.
 Library was size-selected for >1 kb fragments. A
 normalized version of this library is also available
 (NIH_ZGC_7). Library was constructed by Open Biosystems
 (Huntsville, AL)."

ORIGIN

Query Match 92.3%; Score 149.6; DB 14; Length 787;
 Best Local Similarity 97.4%; Pred. No. 1.7e-19; Indels 0; Gaps 0;
 Matches 152; Conservative 0; Mismatches 4;
 QY 6 TACAGGTCACCTAATACCATCTAAGTAGTTCATAGTCACTAGTGCATATGTTGTTTAA 65
 Db 39 TACAGGTCACCTAATACCATCTAAGTAGTTCATAGTGCATATGTTGTTTAA 98
 QY 66 CAGTATTATGATGCTGTTTTTATGCAAAATCTAATTTAATATATGATTTATATCA 125
 Db 99 CAGTATTATGATGCTGTTTTTATGCAAAATCTAATTTAATATATGATTTATATCA 158
 QY 126 TTTTACGTTCTCGTTCAGCTTTTTTATCTAACTT 161
 Db 159 TTTTACGTTCTCGTTCAGCTTTTTTATCTAACTT 194

RESULT 8
 CF347718
 LOCUS 755 bp mRNA linear EST 18-AUG-2003
 DEFINITION AGENCOURT_15225501 NIH_ZGC_10 Danio rerio cDNA clone IMAGE:7001611
 5', mRNA sequence.
 ACCESSION CF347718
 VERSION CF347718.1 GI:33790878
 KEYWORDS EST.
 SOURCE Danio rerio (zebrafish)
 ORGANISM Danio rerio
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Actinopterygii; Neopterygii; Teleostei; Ostariophysi;
 Cypriniformes; Cyprinidae; Danio.
 1 (bases 1 to 755)
 NIH-MGC http://mgs.nci.nih.gov/.
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)
 CONTACT: Daniela S. Gerhard, Ph.D.
 Office of Cancer Genomics
 National Cancer Institute / NIH
 Bldg. 31 Rm10A07 Bethesda, MD 20892
 Email: cgapbs-remail.nih.gov
 Tissue Procurement: Len Zon, Harvard
 cDNA Library Preparation: Open Biosystems
 DNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
 http://image.llnl.gov

FEATURES

source

Plate: LLAM14695 row: c column: 18
 High quality sequence stop: 184.
 Location/Qualifiers
 1. .755

/organism="Danio rerio"
 /mol_type="mRNA"
 /db_xref="taxon:7955"
 /clone="IMAGE:7001611"
 /tissue_type="whole body"
 /lab_host="DH10B"
 /clone_lib="NIH_ZGC_10"
 /notes="Vector: pExpress1; Site 1: NotI; Site 2: EcoRV;
 Bulk tissue was collected from a whole adult individual
 from the Tuebingen strain. 1st strand cDNA was primed with
 a Not I - oligo(dT) primer, double-stranded cDNA was
 cloned into the Not I and EcoRV sites of pExpress-1.
 Library was size-selected for >1 kb fragments. A
 normalized version of this library is also available
 (NIH_ZGC_7). Library was constructed by Open Biosystems
 (Huntsville, AL)."

ORIGIN

Query Match 92.0%; Score 149; DB 14; Length 755;
 Best Local Similarity 96.8%; Pred. No. 2.2e-19; Indels 0; Gaps 0;
 Matches 152; Conservative 0; Mismatches 5;
 QY 6 TACAGGTCACCTAATACCATCTAAGTAGTTCATAGTCACTAGTGCATATGTTGTTTAA 65
 Db 39 TACAGGTCACCTAATACCATCTAAGTAGTTCATAGTCACTAGTGCATATGTTGTTTAA 98
 QY 66 CAGTATTATGATGCTGTTTTTATGCAAAATCTAATTTAATATATGATTTATATCA 125
 Db 99 CAGTATTATGATGCTGTTTTTATGCAAAATCTAATTTAATATATGATTTATATCA 158
 QY 126 TTTTACGTTCTCGTTCAGCTTTTTTATCTAACTT 162
 Db 159 TTTTACGTTCTCGTTCAGCTTTTTTATCTAACTT 195

RESULT 9

AQ991732
 LOCUS 756 bp DNA linear GSS 14-AUG-2000
 DEFINITION RfC00380F Photorhabdus luminescens strain W14 M13 library
 Photorhabdus luminescens genomic clone PLG00380F, genomic survey
 sequence.
 ACCESSION AQ991732
 VERSION AQ991732.1 GI:9650228
 KEYWORDS GSS.
 SOURCE Photorhabdus luminescens
 ORGANISM Photorhabdus luminescens
 Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 Enterobacteriaceae; Photorhabdus.
 1 (bases 1 to 756)
 ffrench-Constant, R.H., Waterfield, N., Burland, V., Perna, N.T.,
 Daborn, P.J., Bowen, D. and Blattner, F.R.
 A genomic sample sequence of the entomopathogenic bacterium
 Photorhabdus luminescens W14: potential implications for virulence
 Appl. Environ. Microbiol. 66 (8), 3310-3329 (2000)
 20378633
 10919786
 CONTACT: ffrench-Constant RH
 Department of Biology and Biochemistry
 University of Bath
 South Building, Bath BA2 7AY, UK
 Tel: (44) 1225 826621
 Fax: (44) 1225 826779
 Email: bssr@bath.ac.uk
 This is one of a selected subset of flipped clones from the M13
 library. For annotation of identified clones (BLASTX, BLASTN and
 mapping to E. coli K12 genome) please see ffrench-Constant et al.
 2000, Nucleic Acids Res.
 Seq primer: M13 Reverse
 Class: shotgun.

FEATURES

source

1. .756
 /organism="Photorhabdus luminescens"
 /mol_type="genomic DNA"

Library was size-selected for >1 kb fragments. A normalized version of this library is also available (NIH ZGC 7). Library was constructed by Open Biosystems (Huntsville, AL)."

ORIGIN

Query Match 85.1%; Score 137.8; DB 14; Length 777;

CF347686

LOCUS

VERSION

KEYWORDS

ORGANIS

AUTHORS

JOURNAL
COMMENT

FEATURES

2

Query Match 83.1%; Score 134.6; DB 14; Length 583;
 Best Local Similarity 97.2%; Pred. No. 1.4e-16;
 Matches 137; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 TCTGTTACAGGTCACATAATACCACTCTAAGTAGTTGATTCATAGTAGCTGCATATGTTGTG 60
 |||||
 DB 141 TCAGTACAGGTCACATATACCATCTAAGTAGTTGATTCATAGTAGCTGCATATGTTGTG 82
 |||||

QY 61 TTTTACAGTATTATGATGCTGTTTTTATGCAAAATCTAATTTAAATATATGATATTTA 120
 |||||
 DB 81 TTTTACAGTATTATGATGCTGTTTTTATGCAAAATCTAATTTAAATATATGATATTTA 22
 |||||

QY 121 TATCATTTTACGTTCTTCGTT 141
 |||||
 DB 21 TATCATTTTACGTTCTTCGTT 1
 |||||

RESULT 12
 AQ991303/c
 LOCUS AQ991303 395 bp DNA linear GSS 14-AUG-2000
 DEFINITION R02205 Photorhabdus luminescens strain W14 M13 library
 Photorhabdus luminescens genomic clone PLG02205, genomic survey
 sequence.
 ACCESSION AQ991303
 VERSION AQ991303.1 GI:9649897
 KEYWORDS GSS.
 SOURCE Photorhabdus luminescens
 ORGANISM Photorhabdus luminescens
 Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 Enterobacteriaceae; Photorhabdus.
 REFERENCE 1 (bases 1 to 395)
 AUTHORS ffrench-Constant,R.H., Waterfield,N., Burland,V., Perna,N.T.,
 Daborn,P.J., Bowen,D. and Blattner,F.R.
 TITLE A genomic sample sequence of the entomopathogenic bacterium
 Photorhabdus luminescens W14: potential implications for virulence
 Appl. Environ. Microbiol. 66 (8), 3310-3329 (2000)
 MEDLINE 20378633
 PUBMED 10919786
 COMMENT Contact: ffrench-Constant RH
 Department of Biology and Biochemistry
 University of Bath
 South Building, Bath BA2 7AY, UK
 Tel: (44) 1225 826521
 Fax: (44) 1225 826779
 Email: bsr1c@bath.ac.uk
 This is one of 2,122 random reads from the M13 library. For
 annotation of identified clones (BLASTX, BLASTN and mapping to E.
 coli K12 genome) please see ffrench-Constant et al. 2000, Nucleic
 Acids Res.
 Seq primer: M13 Forward
 Class: shotgun.
 FEATURES
 source
 1. .395
 Location/Qualifiers
 /organism="Photorhabdus luminescens"
 /mol_type="genomic DNA"
 /strain="W14"
 /db_xref="taxon:29488"
 /clone="PLG02205"
 /dev_stage="primary phase variant"
 /clone_lib="Photorhabdus luminescens strain W14 M13
 library"
 /note="Genomic DNA from strain W14 was size selected (1-2
 kb) and then cloned into M13 Janus."

ORIGIN
 Query Match 82.6%; Score 133.8; DB 28; Length 395;
 Best Local Similarity 91.2%; Pred. No. 2.2e-16;
 Matches 146; Conservative 0; Mismatches 13; Indels 1; Gaps 1;

QY 3 TGTTCAGGTCACATAATACCACTCTAAGTAGTTGATTCATAGTAGCTGCATATGTTGTT 62
 |||||
 DB 345 TGTTCAGGTCACATAATACCACTCTAAGTAGTTGATTCATAGTAGCTGCATATGTTGTT 287
 |||||

QY 63 TTACAGTATTATCTAGTCTGTTTTTATGCAAAATCTAATTTAAATATATGATATTTATA 122
 |||||
 DB 286 TTACAGTATTATCTAGTCTGTTTTTATGCAAAATCTAATTTAAATATATGATATTTATA 227
 |||||

QY 123 TCATTTTACGTTCTCGTTCCAGTCTTTTATATCACTAACCTTG 162
 |||||
 DB 226 TCATTTTACGTTCTCGTTCCAGTCTTTTATATCACTAACCTTG 187
 |||||

RESULT 13
 CB403984/c
 LOCUS CB403984 393 bp mRNA linear EST 15-MAY-2003
 DEFINITION OSTR015E7_1 AD-wrmcDNA Caenorhabditis elegans cDNA, mRNA sequence.
 ACCESSION CB403984
 VERSION CB403984.1 GI:30745711
 KEYWORDS EST.
 SOURCE Caenorhabditis elegans
 ORGANISM Caenorhabditis elegans
 Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida;
 Rhabditidae; Rhabditidae; Peloderinae; Caenorhabditis.
 REFERENCE 1 (bases 1 to 393)
 AUTHORS Reboul,J., Vaglio,P., Rual,J.F., Lamesch,P., Martinez,M.,
 Armstrong,C.M., Li,S., Jacotot,L., Bertin,N., Janky,R., Moore,T.,
 Hudson,J.R., Hartley,J.L., Brasch,M.A., Vandenhaute,J., Boulton,S.,
 Endress,G.A., Jenna,S., Chevet,E., Papasotiropoulos,V.,
 Tollas,P.P., Placek,J., Snyder,M., Huang,R., Chance,M.R., Lee,H.,
 Doucette-Stamm,L., Hill,D.E. and Vidal,M.
 TITLE C. elegans ORFome version 1.1: experimental verification of the
 genome annotation and resource for proteome-scale protein
 expression
 JOURNAL Nat. Genet. (2003) In press
 COMMENT Contact: Vidal M
 Marc Vidal Laboratory
 Dana Farber Cancer Institute
 1 Jimmy Fund Way Smith 858, BOSTON, MA 02115, USA
 Tel: 617 632 5180
 Fax: 617 632 5739
 Email: Marc.Vidal@dfci.harvard.edu
 Sequence tag of Gateway entry clones. The primers used were
 designed on the predicted protein encoding ORF. C. elegans ORFome
 cloning project : Contact david_hill@dfci.harvard.edu or
 marc_vidal@dfci.harvard.edu
 POLYA-No. Location/Qualifiers
 1. .393
 /organism="Caenorhabditis elegans"
 /mol_type="mRNA"
 /strain="N2"
 /db_xref="taxon:6239"
 /sex="Hermaphrodite and male"
 /tissue_type="whole animal"
 /dev_stage="mixed stage"
 /clone_lib="AD-wrmcDNA"
 /note="The AD-wrmcDNA library was generated with poly(A) +
 RNA isolated from both hermaphrodite and male N2 worms of
 all larval stages, embryos, adults and dauers and the
 subsequent generation of cDNAs by poly(A) priming. The
 cDNAs were cloned into pPC96"

ORIGIN
 Query Match 80.1%; Score 129.8; DB 14; Length 393;
 Best Local Similarity 95.0%; Pred. No. 1.3e-15;
 Matches 134; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 1 TCTGTTACAGGTCACATAATACCACTCTAAGTAGTTGATTCATAGTAGCTGCATATGTTGTG 60
 |||||
 DB 141 TCAGTACAGGTCACATAATACCACTCTAAGTAGTTGATTCATAGTAGCTGCATATGTTGTG 82
 |||||

QY 61 TTTTACAGTATTATGATGCTGTTTTTATGCAAAATCTAATTTAAATATATGATATTTA 120
 |||||
 DB 81 TTTTACAGTATTATGATGCTGTTTTTATGCAAAATCTAATTTAAATATATGATATTTA 22
 |||||

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QY 121 TATCATTTTACGTTTCTCGTT 141
Db 21 TATCATCTCAGCTTCTCGTT 1

RESULT 14
AQ990470/c
LOCUS
DEFINITION
  769 bp DNA linear GSS 14-AUG-2000
  Rfc01245 Photorhabdus luminescens strain W14 M13 library
  Photorhabdus luminescens genomic clone PLG01245, genomic survey
  sequence.
ACCESSION
  AQ990470
VERSION
  AQ990470.1 GI:9649064
KEYWORDS
  GSS.
SOURCE
  Photorhabdus luminescens
  Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
  Enterobacteriaceae; Photorhabdus.
REFERENCE
  1 (bases 1 to 769)
  ffrench-Constant,R.H., Waterfield,N., Burland,V., Perna,N.T.,
  Daborn,P.J., Bowen,D. and Blattner,F.R.
  A genomic sample sequence of the entomopathogenic bacterium
  Photorhabdus luminescens W14: potential implications for virulence
  Appl. Environ. Microbiol. 66 (8), 3310-3329 (2000)
  20378633
PUBMED
  10919786
COMMENT
  Contact: ffrench-Constant RH
  Department of Biology and Biochemistry
  University of Bath
  South Building, Bath BA2 7AY, UK
  Tel: (44) 1225 826621
  Fax: (44) 1225 826779
  Email: bssrfc@bath.ac.uk
  This is one of 2,122 random reads from the M13 library. For
  annotation of identified clones (BLASTX, BLASTN and mapping to E.
  coli K12 genome) please see ffrench-Constant et al. 2000, Nucleic
  Acids Res.
  Seq primer: M13 Forward
  Class: shotgun.
  Location/Qualifiers
    1..769
    /organism="Photorhabdus luminescens"
    /mol_type="genomic DNA"
    /strain="W14"
    /db_xref="taxon:29488"
    /clone="PLG01245"
    /dev_stage="primary phase variant"
    /clone_lib="Photorhabdus luminescens strain W14 M13
    library"
    /note="Genomic DNA from strain W14 was size selected (1-2
    kb) and then cloned into M13 Janus."

ORIGIN
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Best Local Similarity 90.7%; Pred. No. 1.6e-15;
Matches 147; Conservative 0; Mismatches 14; Indels 1; Gaps 1;

QY 2 CTGTTACAGGTCACATAATACCATCTAAGTAGTTGATTCATAGTCACTGCATATGTTGTG 61
Db 769 CTGTACAGGTCACATATCCCATTTAAAGTAGTTGATTCATAGTCACTGCATATGTTGTG 710

QY 62 TTTCAGATTAATGATGCTGTTTTTATGCAAAATCTAATTTAATATATATGATATTAT 121
Db 709 TTNACAGTATATGATGCTGTTTTTATGCAAAATCTAATTTAATATATGATATTAT 550

QY 122 ATCATTTACGTTTC-TGCTTCAGCTTTTTTATACAACTTG 162
Db 649 ATCATTTACGTTTCTCTCGTTTCTCGTTTCTTATACAACTTG 608

RESULT 15
AQ990878/c
LOCUS
DEFINITION
  764 bp DNA linear GSS 14-AUG-2000
  Rfc01715 Photorhabdus luminescens strain W14 M13 library
  Photorhabdus luminescens genomic clone PLG01715, genomic survey
  sequence.
ACCESSION
  AQ990878
VERSION
  AQ990878.1 GI:9649472
KEYWORDS
  GSS.
SOURCE
  Photorhabdus luminescens
  Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
  Enterobacteriaceae; Photorhabdus.
REFERENCE
  1 (bases 1 to 764)
  ffrench-Constant,R.H., Waterfield,N., Burland,V., Perna,N.T.,
  Daborn,P.J., Bowen,D. and Blattner,F.R.
  A genomic sample sequence of the entomopathogenic bacterium
  Photorhabdus luminescens W14: potential implications for virulence
  Appl. Environ. Microbiol. 66 (8), 3310-3329 (2000)
  20378633
PUBMED
  10919786
COMMENT
  Contact: ffrench-Constant RH
  Department of Biology and Biochemistry
  University of Bath
  South Building, Bath BA2 7AY, UK
  Tel: (44) 1225 826621
  Fax: (44) 1225 826779
  Email: bssrfc@bath.ac.uk
  This is one of 2,122 random reads from the M13 library. For
  annotation of identified clones (BLASTX, BLASTN and mapping to E.
  coli K12 genome) please see ffrench-Constant et al. 2000, Nucleic
  Acids Res.
  Seq primer: M13 Forward
  Class: shotgun.
  Location/Qualifiers
    1..764
    /organism="Photorhabdus luminescens"
    /mol_type="genomic DNA"
    /strain="W14"
    /db_xref="taxon:29488"
    /clone="PLG01715"
    /dev_stage="primary phase variant"
    /clone_lib="Photorhabdus luminescens strain W14 M13
    library"
    /note="Genomic DNA from strain W14 was size selected (1-2
    kb) and then cloned into M13 Janus."

ORIGIN
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Best Local Similarity 95.9%; Pred. No. 5.1e-15;
Matches 139; Conservative 0; Mismatches 5; Indels 1; Gaps 1;

QY 6 TACAGGTCACATAATACCATCTAAGTAGTTGATTCATAGTCACTGCATATGTTGTGTTTA 65
Db 763 TACAGGTCACATAAACCATTAAAGTAGTTGATTCATAGTCCGCATATGTTGTGTTTA 704

QY 66 CAGTATTATGATGCTGTTTTTATGCAAAATCTAATTTAATATATGATATTATATCA 125
Db 703 CAGTATTATGATGCTGTTTTTATGCAAAATCTAATTTAATATATGATATTATCA 645

QY 126 TTTACGTTTCTCGTTTCAGCTTTT 150
Db 644 TTTACGTTTCTCGTTTCAGCTTTT 620

Search completed: September 9, 2004, 21:18:25
Job time : 1309.61 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: September 9, 2004, 19:34:38 ; Search time 204.654 Seconds
(without alignments)
3982.858 Million cell updates/sec

Title: US-10-082-772B-4

Perfect score: 162
Sequence: 1 tctgttagcagtcactaata.....agctttttatactaacttg 162

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 3304383 seqs, 2515761380 residues

Total number of hits satisfying chosen parameters: 6608766

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications NA:*

- 1: /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq.*
- 2: /cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq.*
- 3: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq.*
- 4: /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq.*
- 5: /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq.*
- 6: /cgn2_6/ptodata/2/pubpna/PCTUS_PUBCOMB.seq.*
- 7: /cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq.*
- 8: /cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq.*
- 9: /cgn2_6/ptodata/2/pubpna/US09A_PUBCOMB.seq.*
- 10: /cgn2_6/ptodata/2/pubpna/US09B_PUBCOMB.seq.*
- 11: /cgn2_6/ptodata/2/pubpna/US09C_PUBCOMB.seq.*
- 12: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq.*
- 13: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq2.*
- 14: /cgn2_6/ptodata/2/pubpna/US10A_PUBCOMB.seq.*
- 15: /cgn2_6/ptodata/2/pubpna/US10B_PUBCOMB.seq.*
- 16: /cgn2_6/ptodata/2/pubpna/US10C_PUBCOMB.seq.*
- 17: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq.*
- 18: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq.*
- 19: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	162	100.0	162	17	US-10-310-695-16
2	162	100.0	166	13	US-10-403-232-175
3	162	100.0	168	17	US-10-627-711-10
4	160.4	99.0	243	13	US-10-403-232-173
5	160.4	99.0	243	17	US-10-310-695-14
6	160.4	99.0	248	17	US-10-627-711-8
7	160.4	99.0	282	15	US-10-161-403-72
8	160.4	99.0	1763	11	US-09-244-805-57
9	160.4	99.0	1763	11	US-09-245-277-57
10	160.4	99.0	1763	17	US-10-792-481-57
11	160.4	99.0	4346	15	US-10-161-403-113
12	155.6	96.0	243	17	US-10-310-695-2
13	152.4	94.1	17458	15	US-10-055-001A-25
14	152.4	94.1	17458	15	US-10-055-001A-25

15	152.4	94.1	17476	15	US-10-055-001A-24	Sequence 24, Appl
16	152.4	94.1	17476	15	US-10-055-001A-24	Sequence 24, Appl
17	152.4	94.1	17476	15	US-10-385-546-7	Sequence 7, Appl
18	152.4	94.1	17476	15	US-10-385-546-7	Sequence 7, Appl
19	152.4	94.1	17681	15	US-10-055-001A-26	Sequence 26, Appl
20	152.4	94.1	17681	15	US-10-055-001A-26	Sequence 26, Appl
21	152.2	94.0	158	13	US-10-403-232-181	Sequence 181, Appl
22	150.8	93.1	4470	15	US-10-151-690-21	Sequence 21, Appl
23	150.8	93.1	4892	16	US-10-357-268-1	Sequence 1, Appl
24	150.8	93.1	5584	15	US-10-151-690-61	Sequence 61, Appl
25	150.8	93.1	17862	15	US-10-055-001A-23	Sequence 23, Appl
26	150.8	93.1	17862	15	US-10-055-001A-23	Sequence 23, Appl
27	150.8	93.1	18691	15	US-10-055-001A-13	Sequence 13, Appl
28	150.8	93.1	18691	15	US-10-055-001A-13	Sequence 13, Appl
29	150.6	93.0	233	13	US-10-301-849A-16	Sequence 16, Appl
30	150.6	93.0	233	13	US-10-403-232-177	Sequence 177, Appl
31	149.2	92.1	4428	15	US-10-151-690-62	Sequence 62, Appl
32	149.2	92.1	4470	15	US-10-151-690-21	Sequence 21, Appl
33	149.2	92.1	4627	15	US-10-151-690-63	Sequence 63, Appl
34	149.2	92.1	4627	15	US-10-151-690-64	Sequence 64, Appl
35	149.2	92.1	4892	16	US-10-357-268-1	Sequence 1, Appl
36	149.2	92.1	5584	15	US-10-151-690-61	Sequence 61, Appl
37	149	92.0	233	13	US-10-403-232-179	Sequence 179, Appl
38	148.4	91.6	2959	13	US-10-270-176-8	Sequence 8, Appl
39	148.4	91.6	3663	13	US-10-270-176-3	Sequence 3, Appl
40	148.4	91.6	3695	13	US-10-270-176-13	Sequence 13, Appl
41	148.4	91.6	4782	13	US-10-270-176-20	Sequence 20, Appl
42	148.4	91.6	5646	13	US-10-270-176-41	Sequence 41, Appl
43	148.4	91.6	5706	13	US-10-270-176-40	Sequence 40, Appl
44	148.4	91.6	5739	13	US-10-270-176-9	Sequence 9, Appl
45	148.4	91.6	5771	13	US-10-270-176-34	Sequence 34, Appl

ALIGNMENTS

RESULT 1

US-10-310-695-16
; Sequence 16, Application US/10310695
; Publication No. US20040110293A1
; GENERAL INFORMATION:
; APPLICANT: DROGE, PETER
; APPLICANT: ENENKEL, BARBARA
; TITLE OF INVENTION: SEQUENCE SPECIFIC DNA RECOMBINATION IN EUKARYOTIC CELLS
; FILE REFERENCE: DEEE:0190US
; CURRENT APPLICATION NUMBER: US/10/310,695
; CURRENT FILING DATE: 2002-12-05
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 16
; LENGTH: 162
; TYPE: DNA
; ORGANISM: Escherichia coli
US-10-310-695-16

Query Match 100.0%; Score 162; DB 17; Length 162;
Best Local Similarity 100.0%; Pred. NO. 1.3e-25;
Matches 162; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	TCTGTTACAGTCTACTAATACCATCTAAGTAGTTGATTGACTGACTGATGTTGTG	60
Db	1	TCTGTTACAGTCTACTAATACCATCTAAGTAGTTGATTGACTGACTGATGTTGTG	60
Qy	61	TTTTACAGTATTATGATGTCGTTTTTTATGCAAAATCTAATTAATATATGATATTTA	120
Db	61	TTTTACAGTATTATGATGTCGTTTTTTATGCAAAATCTAATTAATATATGATATTTA	120
Qy	121	TATCATTTTACGTTCTCGTTTCAGCTTTTATATCTAACTTGG	162
Db	121	TATCATTTTACGTTCTCGTTTCAGCTTTTATATCTAACTTGG	162

RESULT 2

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US-10-403-232-175
; Sequence 175, Application US/10403232
; Publication No. US20030226164A1
; GENERAL INFORMATION:
; APPLICANT: Suttie, Janet Louise
; APPLICANT: Chilton, Mary-Dell
; APPLICANT: Que, Quideng
; APPLICANT: de Ramond, Anic
; TITLE OF INVENTION: Lambda Integrase Mediated Recombination In Plants
; FILE REFERENCE: 70005USPS
; CURRENT APPLICATION NUMBER: US/10/403,232
; CURRENT FILING DATE: 2003-03-28
; NUMBER OF SEQ ID NOS: 185
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 175
; LENGTH: 166
; TYPE: DNA
; ORGANISM: Bacteriophage lambda
US-10-403-232-175

Query Match      100.0%; Score 162; DB 13; Length 166;
Best Local Similarity 100.0%; Pred. No. 1.4e-25;
Matches 162; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCTGTTACAGGTCACCTAATACCATCTAAGTAGTGTGATTCATAGTGACTGCATATGTTGG 60
Db 1 TCTGTTACAGGTCACCTAATACCATCTAAGTAGTGTGATTCATAGTGACTGCATATGTTGG 60
QY 61 TTTTACAGTATTATGAGTCTGTTTTATGCAAAATCTAAATTAATATATGATATTTA 120
Db 61 TTTTACAGTATTATGAGTCTGTTTTATGCAAAATCTAAATTAATATATGATATTTA 120
QY 121 TATCATTTTACGTTTCTCGTTACGCTTTTATATACTAAGTTG 162
Db 121 TATCATTTTACGTTTCTCGTTACGCTTTTATATACTAAGTTG 162

RESULT 3
US-10-627-711-10
; Sequence 10, Application US/10627711
; Publication No. US20040115812A1
; GENERAL INFORMATION:
; APPLICANT: YANG, Shuwei
; TITLE OF INVENTION: METHODS AND NUCLEIC ACID VECTORS FOR RAPID EXPRESSION AND
; FILE REFERENCE: 51236US
; CURRENT APPLICATION NUMBER: US/10/627,711
; CURRENT FILING DATE: 2003-07-28
; PRIOR APPLICATION NUMBER: 60/398,589
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 10
; LENGTH: 168
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: primer
US-10-627-711-10

Query Match      100.0%; Score 162; DB 17; Length 168;
Best Local Similarity 100.0%; Pred. No. 1.4e-25;
Matches 162; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCTGTTACAGGTCACCTAATACCATCTAAGTAGTGTGATTCATAGTGACTGCATATGTTGG 60
Db 6 TCTGTTACAGGTCACCTAATACCATCTAAGTAGTGTGATTCATAGTGACTGCATATGTTGG 65
QY 61 TTTTACAGTATTATGAGTCTGTTTTATGCAAAATCTAAATTAATATATGATATTTA 120
Db 66 TTTTACAGTATTATGAGTCTGTTTTATGCAAAATCTAAATTAATATATGATATTTA 125
QY 121 TATCATTTTACGTTTCTCGTTACGCTTTTATATACTAAGTTG 162

US-10-403-232-173
; Sequence 173, Application US/10403232
; Publication No. US20030226164A1
; GENERAL INFORMATION:
; APPLICANT: Suttie, Janet Louise
; APPLICANT: Chilton, Mary-Dell
; APPLICANT: Que, Quideng
; APPLICANT: de Ramond, Anic
; TITLE OF INVENTION: Lambda Integrase Mediated Recombination In Plants
; FILE REFERENCE: 70005USPS
; CURRENT APPLICATION NUMBER: US/10/403,232
; CURRENT FILING DATE: 2003-03-28
; NUMBER OF SEQ ID NOS: 185
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 173
; LENGTH: 243
; TYPE: DNA
; ORGANISM: Bacteriophage lambda
US-10-403-232-173

Query Match      99.0%; Score 160.4; DB 13; Length 243;
Best Local Similarity 99.4%; Pred. No. 3.3e-25;
Matches 161; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TCTGTTACAGGTCACCTAATACCATCTAAGTAGTGTGATTCATAGTGACTGCATATGTTGG 60
Db 1 TCTGTTACAGGTCACCTAATACCATCTAAGTAGTGTGATTCATAGTGACTGCATATGTTGG 60
QY 61 TTTTACAGTATTATGAGTCTGTTTTATGCAAAATCTAAATTAATATATGATATTTA 120
Db 61 TTTTACAGTATTATGAGTCTGTTTTATGCAAAATCTAAATTAATATATGATATTTA 120
QY 121 TATCATTTTACGTTTCTCGTTACGCTTTTATATACTAAGTTG 162
Db 121 TATCATTTTACGTTTCTCGTTACGCTTTTATATACTAAGTTG 162

RESULT 5
US-10-310-695-14
; Sequence 14, Application US/10310695
; Publication No. US20040110293A1
; GENERAL INFORMATION:
; APPLICANT: ENENKEL, BARBARA
; APPLICANT: DROGE, PETER
; TITLE OF INVENTION: SEQUENCE SPECIFIC DNA RECOMBINATION IN EUKARYOTIC CELLS
; FILE REFERENCE: DEBE:019US
; CURRENT APPLICATION NUMBER: US/10/310,695
; CURRENT FILING DATE: 2002-12-05
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 14
; LENGTH: 243
; TYPE: DNA
; ORGANISM: Bacteriophage lambda
US-10-310-695-14

Query Match      99.0%; Score 160.4; DB 17; Length 243;
Best Local Similarity 99.4%; Pred. No. 3.3e-25;
Matches 161; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TCTGTTACAGGTCACCTAATACCATCTAAGTAGTGTGATTCATAGTGACTGCATATGTTGG 60
Db 1 TCTGTTACAGGTCACCTAATACCATCTAAGTAGTGTGATTCATAGTGACTGCATATGTTGG 60
QY 61 TTTTACAGTATTATGAGTCTGTTTTATGCAAAATCTAAATTAATATATGATATTTA 120
Db 61 TTTTACAGTATTATGAGTCTGTTTTATGCAAAATCTAAATTAATATATGATATTTA 120
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QY 121 TATCAATTTACGTTCTCGTTACGCTTTTATATACAACTTG 162
Db 121 TATCAATTTACGTTCTCGTTACGCTTTTATATACAACTTG 162

RESULT 6
US-10-627-711-8
; Sequence 8, Application US/10627711
; Publication No. US20040115812A1
; GENERAL INFORMATION:
; APPLICANT: YANG, Shuwei
; TITLE OF INVENTION: METHODS AND NUCLEIC ACID VECTORS FOR RAPID EXPRESSION AND
; FILE REFERENCE: 51236US
; CURRENT APPLICATION NUMBER: US/10/627,711
; PRIOR FILING DATE: 2003-07-28
; PRIOR APPLICATION NUMBER: 60/398,589
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 8
; LENGTH: 248
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: primer
US-10-627-711-8

Query Match 99.0%; Score 160.4; DB 17; Length 248;
Best Local Similarity 99.4%; Pred. No. 3.3e-25;
Matches 161; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TCTGTTACAGTCACTAATACCATCTAAGTAGTGTGATCATAGTGCATGATGTTGTG 60
Db 6 TCTGTTACAGTCACTAATACCATCTAAGTAGTGTGATCATAGTGCATGATGTTGTG 65
QY 61 TTTTACAGTATTAGTAGTCTGTTTTATGCAAAATCTAATTAATATATGATATTTA 120
Db 66 TTTTACAGTATTAGTAGTCTGTTTTATGCAAAATCTAATTAATATATGATATTTA 125
QY 121 TATCAATTTACGTTCTCGTTACGCTTTTATATACAACTTG 162
Db 126 TATCAATTTACGTTCTCGTTACGCTTTTATATACAACTTG 167

RESULT 7
US-10-161-403-72
; Sequence 72, Application US/10161403
; Publication No. US20030119104A1
; GENERAL INFORMATION:
; APPLICANT: Perkins, Edward
; APPLICANT: Perez, Carl
; APPLICANT: Lindenbaum, Michael
; APPLICANT: Greene, Amy
; APPLICANT: Leung, Josephine
; APPLICANT: Fleming, Elena
; APPLICANT: Stewart, Sandra
; APPLICANT: Shellard, Joan
; TITLE OF INVENTION: CHROMOSOME-BASED PLATFORMS
; FILE REFERENCE: 24601-420
; CURRENT APPLICATION NUMBER: US/10/161,403
; CURRENT FILING DATE: 2002-05-30
; PRIOR FILING DATE: 2001-05-30
; PRIOR APPLICATION NUMBER: 60/366,891
; PRIOR FILING DATE: 2002-03-21
; NUMBER OF SEQ ID NOS: 129
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 72
; LENGTH: 282
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
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; OTHER INFORMATION: attp
US-10-161-403-72

Query Match 99.0%; Score 160.4; DB 15; Length 282;
Best Local Similarity 99.4%; Pred. No. 3.5e-25;
Matches 161; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TCTGTTACAGTCACTAATACCATCTAAGTAGTGTGATCATAGTGCATGATGTTGTG 60
Db 15 TCTGTTACAGTCACTAATACCATCTAAGTAGTGTGATCATAGTGCATGATGTTGTG 74
QY 61 TTTTACAGTATTAGTAGTCTGTTTTATGCAAAATCTAATTAATATATGATATTTA 120
Db 75 TTTTACAGTATTAGTAGTCTGTTTTATGCAAAATCTAATTAATATATGATATTTA 134
QY 121 TATCAATTTACGTTCTCGTTACGCTTTTATATACAACTTG 162
Db 135 TATCAATTTACGTTCTCGTTACGCTTTTATATACAACTTG 176

RESULT 8
US-09-244-805-57/c
; Sequence 57, Application US/09244805
; Publication No. US20030203840A1
; GENERAL INFORMATION:
; APPLICANT: Worley, Paul F.
; APPLICANT: Lanahan, Anthony
; APPLICANT: Goetz, Bernard
; APPLICANT: Heimisch, Holger
; APPLICANT: Kuner, Rohini
; APPLICANT: Scheek, Sigrid
; APPLICANT: Nikolich, Karoly
; APPLICANT: Zhukowski, Eugene
; TITLE OF INVENTION: IMMEDIATE EARLY GENES AND METHODS OF USE
; FILE REFERENCE: 10496/004001
; CURRENT APPLICATION NUMBER: US/09/244,805
; CURRENT FILING DATE: 1999-02-05
; EARLIER APPLICATION NUMBER: 60/074,518
; EARLIER FILING DATE: 1998-02-12
; EARLIER APPLICATION NUMBER: 60/074,135
; EARLIER FILING DATE: 1998-02-06
; NUMBER OF SEQ ID NOS: 62
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 57
; LENGTH: 1763
; TYPE: DNA
; ORGANISM: Eukaryote
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(1763)
; OTHER INFORMATION: Y = C or T
; OTHER INFORMATION: n = A,T,C or G
US-09-244-805-57

Query Match 99.0%; Score 160.4; DB 11; Length 1763;
Best Local Similarity 99.4%; Pred. No. 5.9e-25;
Matches 161; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TCTGTTACAGTCACTAATACCATCTAAGTAGTGTGATCATAGTGCATGATGTTGTG 60
Db 431 TCTGTTACAGTCACTAATACCATCTAAGTAGTGTGATCATAGTGCATGATGTTGTG 372
QY 61 TTTTACAGTATTAGTAGTCTGTTTTATGCAAAATCTAATTAATATATGATATTTA 120
Db 371 TTTTACAGTATTAGTAGTCTGTTTTATGCAAAATCTAATTAATATATGATATTTA 312
QY 121 TATCAATTTACGTTCTCGTTACGCTTTTATATACAACTTG 162
Db 311 TATCAATTTACGTTCTCGTTACGCTTTTATATACAACTTG 270

RESULT 9
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US-09-245-277-57/c
; Sequence 57, Application US/09245277
; Publication No. US20030211984A1
; GENERAL INFORMATION:
; APPLICANT: Worley, Paul F.
; APPLICANT: Lanahan, Anthony
; TITLE OF INVENTION: IMMEDIATE EARLY GENES AND METHODS OF USE
; TITLE OF INVENTION: THEREFOR
; FILE REFERENCE: JHUL530-3
; CURRENT APPLICATION NUMBER: US/09/245,277
; CURRENT FILING DATE: 1999-02-05
; PRIOR APPLICATION NUMBER: 60/074,518
; PRIOR FILING DATE: 1998-02-12
; PRIOR APPLICATION NUMBER: 60/074,135
; PRIOR FILING DATE: 1998-02-06
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 57
; LENGTH: 1763
; TYPE: DNA
; ORGANISM: Eukaryote
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)...(1763)
; OTHER INFORMATION: Y = C or T
; OTHER INFORMATION: n = A,T,C or G
US-09-245-277-57

Query Match          99.0%; Score 160.4; DB 11; Length 1763;
Best Local Similarity 99.4%; Pred. No. 5.9e-25;
Matches 161; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1  TCTGTTACAGGTCACCTAAATACCATCTAAGTAGTCTGATTCATTCATAGTGCATGCTGATGTTGTG 60
DB      431 TCTGTTACAGGTCACCTAAATACCATCTAAGTAGTCTGATTCATTCATAGTGCATGCTGATGTTGTG 372

QY      61  TTTTACAGTATTATGTCGTCTGTTTTTATGCAAAATCTAATTTAATATATGATATTTA 120
DB      371 TTTTACAGTATTATGTCGTCTGTTTTTATGCAAAATCTAATTTAATATATGATATTTA 312

QY      121 TATCATTTTACGTTCTCGTTCAGCTTTTTTATATACTAAGTTG 162
DB      311 TATCATTTTACGTTCTCGTTCAGCTTTTTTATATACTAAGTTG 270

RESULT 11
US-10-161-403-113
; Sequence 113, Application US/10161403
; Publication No. US20030119104A1
; GENERAL INFORMATION:
; APPLICANT: Perkins, Edward
; APPLICANT: Perez, Carl
; APPLICANT: Lindenbaum, Michael
; APPLICANT: Greene, Amy
; APPLICANT: Leung, Josephine
; APPLICANT: Fleming, Elena
; APPLICANT: Stewart, Sandra
; APPLICANT: Shellard, Joan
; TITLE OF INVENTION: CHROMOSOME-BASED PLATFORMS
; FILE REFERENCE: 24601-420
; CURRENT APPLICATION NUMBER: US/10/161,403
; CURRENT FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: 60/294,758
; PRIOR FILING DATE: 2001-05-30
; PRIOR APPLICATION NUMBER: 60/366,891
; PRIOR FILING DATE: 2002-03-21
; NUMBER OF SEQ ID NOS: 129
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 113
; LENGTH: 4346
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: pSV40-193AttpsensePur Plasmid
US-10-161-403-113

Query Match          99.0%; Score 160.4; DB 15; Length 4346;
Best Local Similarity 99.4%; Pred. No. 7.6e-25;
Matches 161; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1  TCTGTTACAGGTCACCTAAATACCATCTAAGTAGTCTGATTCATTCATAGTGCATGCTGATGTTGTG 60
DB      4070 TCTGTTACAGGTCACCTAAATACCATCTAAGTAGTCTGATTCATTCATAGTGCATGCTGATGTTGTG 4129

QY      61  TTTTACAGTATTATGTCGTCTGTTTTTATGCAAAATCTAATTTAATATATGATATTTA 120
DB      4130 TTTTACAGTATTATGTCGTCTGTTTTTATGCAAAATCTAATTTAATATATGATATTTA 4189

QY      121 TATCATTTTACGTTTCTCGTTCAGCTTTTTTATATACTAAGTTG 162
DB      4190 TATCATTTTACGTTTCTCGTTCAGCTTTTTTATATACTAAGTTG 4231

US-09-245-277-57/c
; Sequence 57, Application US/10792481
; Publication No. US20040152658A1
; GENERAL INFORMATION:
; APPLICANT: Worley, Paul F.
; APPLICANT: Lanahan, Anthony
; APPLICANT: Goetz, Bernard
; APPLICANT: Heimisch, Holger
; APPLICANT: Kuner, Rohini
; APPLICANT: Scheek, Sigrid
; APPLICANT: Nikolich, Karoly
; APPLICANT: Zhukovski, Eugene
; TITLE OF INVENTION: IMMEDIATE EARLY GENES AND METHODS OF USE
; TITLE OF INVENTION: THEREFOR
; FILE REFERENCE: 10496/004001
; CURRENT APPLICATION NUMBER: US/10/792,481
; CURRENT FILING DATE: 2004-03-02
; PRIOR APPLICATION NUMBER: US/09/244,805
; PRIOR FILING DATE: 1999-02-05
; PRIOR APPLICATION NUMBER: 60/074,518
; PRIOR FILING DATE: 1998-02-12
; PRIOR APPLICATION NUMBER: 60/074,135
; PRIOR FILING DATE: 1998-02-06
; NUMBER OF SEQ ID NOS: 62
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 57
; LENGTH: 1763

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RESULT 12
US-10-310-695-2
; Sequence 2, Application US/10310695
; Publication No. US20040110293A1
; GENERAL INFORMATION:
; APPLICANT: ENENKEL, BARBARA
; TITLE OF INVENTION: SEQUENCE SPECIFIC DNA RECOMBINATION IN EUKARYOTIC CELLS
; FILE REFERENCE: DEBE:0190S
; CURRENT APPLICATION NUMBER: US/10/310,695
; CURRENT FILING DATE: 2002-12-05
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 243
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Primer
US-10-310-695-2

Query Match          96.0%; Score 155.6; DB 17; Length 243;
Best Local Similarity 97.5%; Pred. No. 3.6e-24;
Matches 158; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 TCTGTTACAGGTCACATAATACCATCTAAGTAGTTGATTCATAGTAGCTGCATATGTTGTG 60
Db 1 TCTGTTACAGGTCACATAATACCATCTAAGTAGTTGATTCATAGTAGCTGCATATCTTTGTG 60

QY 61 TTTTACAGTATTATGATGTCGTTTTTATGCAAAATCTAATTAATATATTGATATTTA 120
Db 61 TTTTACAGTATTATGATGTCGTTTTTATGCAAAATCTAATTAATATATTGATATTTA 120

QY 121 TATCAATTTACGTTCTCGTTCAGCTTTTATTAATACTAACTTG 162
Db 121 TATCAATTTACGTTCTCGTTCAGCTTTTATTAATACTAACTTG 162

RESULT 13
US-10-055-001A-25
; Sequence 25, Application US/10055001A
; Publication No. US20030049835A1
; GENERAL INFORMATION:
; APPLICANT: Wesley, Susan V.
; APPLICANT: Waterhouse, Peter
; TITLE OF INVENTION: Method and means for producing efficient silencing constructs
; TITLE OF INVENTION: using recombinational cloning
; FILE REFERENCE: HELIGA
; CURRENT APPLICATION NUMBER: US/10/055,001A
; CURRENT FILING DATE: 2002-06-11
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 25
; LENGTH: 17458
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: acceptor vector pHELLSGATE11
US-10-055-001A-25

Query Match          94.1%; Score 152.4; DB 15; Length 17458;
Best Local Similarity 96.3%; Pred. No. 5.8e-23;
Matches 156; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 TCTGTTACAGGTCACATAATACCATCTAAGTAGTTGATTCATAGTAGCTGCATATGTTGTG 60
Db 1 TCTGTTACAGGTCACATAATACCATCTAAGTAGTTGATTCATAGTAGCTGCATATGTTGTG 60

QY 61 TTTTACAGTATTATGATGTCGTTTTTATGCAAAATCTAATTAATATATTGATATTTA 120
Db 61 TTTTACAGTATTATGATGTCGTTTTTATGCAAAATCTAATTAATATATTGATATTTA 120

QY 121 TATCAATTTACGTTCTCGTTCAGCTTTTATTAATACTAACTTG 162
Db 121 TATCAATTTACGTTCTCGTTCAGCTTTTATTAATACTAACTTG 162

RESULT 14
US-10-055-001A-25/c
; Sequence 25, Application US/10055001A
; Publication No. US20030049835A1
; GENERAL INFORMATION:
; APPLICANT: Wesley, Susan V.
; APPLICANT: Waterhouse, Peter
; APPLICANT: Helliwell, Christopher A.
; TITLE OF INVENTION: Method and means for producing efficient silencing constructs
; TITLE OF INVENTION: using recombinational cloning
; FILE REFERENCE: HELIGA
; CURRENT APPLICATION NUMBER: US/10/055,001A
; CURRENT FILING DATE: 2002-06-11
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 25
; LENGTH: 17458
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: acceptor vector pHELLSGATE11
US-10-055-001A-25

Query Match          94.1%; Score 152.4; DB 15; Length 17458;
Best Local Similarity 96.3%; Pred. No. 5.8e-23;
Matches 156; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 TCTGTTACAGGTCACATAATACCATCTAAGTAGTTGATTCATAGTAGCTGCATATGTTGTG 60
Db 1 TCTGTTACAGGTCACATAATACCATCTAAGTAGTTGATTCATAGTAGCTGCATATGTTGTG 60

QY 61 TTTTACAGTATTATGATGTCGTTTTTATGCAAAATCTAATTAATATATTGATATTTA 120
Db 61 TTTTACAGTATTATGATGTCGTTTTTATGCAAAATCTAATTAATATATTGATATTTA 120

QY 121 TATCAATTTACGTTCTCGTTCAGCTTTTATTAATACTAACTTG 162
Db 121 TATCAATTTACGTTCTCGTTCAGCTTTTATTAATACTAACTTG 162

RESULT 15
US-10-055-001A-24
; Sequence 24, Application US/10055001A
; Publication No. US20030049835A1
; GENERAL INFORMATION:
; APPLICANT: Wesley, Susan V.
; APPLICANT: Waterhouse, Peter
; APPLICANT: Helliwell, Christopher A.
; TITLE OF INVENTION: Method and means for producing efficient silencing constructs
; TITLE OF INVENTION: using recombinational cloning
; FILE REFERENCE: HELIGA
; CURRENT APPLICATION NUMBER: US/10/055,001A
; CURRENT FILING DATE: 2002-06-11
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 24
; LENGTH: 17476
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: acceptor vector pHELLSGATE8
US-10-055-001A-24

Query Match          94.1%; Score 152.4; DB 15; Length 17476;
Best Local Similarity 96.3%; Pred. No. 5.8e-23;
Matches 156; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
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Db 16578 TTTTACAGTATTATGATGTCGTTTTTATGCAAAATCTAATTAATATATTGATATTTA 16637

QY 121 TATCAATTTACGTTCTCGTTCAGCTTTTATTAATACTAACTTG 162
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RESULT 14
US-10-055-001A-25/c
; Sequence 25, Application US/10055001A
; Publication No. US20030049835A1
; GENERAL INFORMATION:
; APPLICANT: Wesley, Susan V.
; APPLICANT: Waterhouse, Peter
; APPLICANT: Helliwell, Christopher A.
; TITLE OF INVENTION: Method and means for producing efficient silencing constructs
; TITLE OF INVENTION: using recombinational cloning
; FILE REFERENCE: HELIGA
; CURRENT APPLICATION NUMBER: US/10/055,001A
; CURRENT FILING DATE: 2002-06-11
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 25
; LENGTH: 17458
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: acceptor vector pHELLSGATE11
US-10-055-001A-25

Query Match          94.1%; Score 152.4; DB 15; Length 17458;
Best Local Similarity 96.3%; Pred. No. 5.8e-23;
Matches 156; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 TCTGTTACAGGTCACATAATACCATCTAAGTAGTTGATTCATAGTAGCTGCATATGTTGTG 60
Db 13188 TCGACTACAGGTCACATAATACCATCTAAGTAGTTGATTCATAGTAGCTGCATATGTTGTG 13129

QY 61 TTTTACAGTATTATGATGTCGTTTTTATGCAAAATCTAATTAATATATTGATATTTA 120
Db 13128 TTTTACAGTATTATGATGTCGTTTTTATGCAAAATCTAATTAATATATTGATATTTA 13069

QY 121 TATCAATTTACGTTCTCGTTCAGCTTTTATTAATACTAACTTG 162
Db 13068 TATCAATTTACGTTCTCGTTCAGCTTTTATTAATACTAACTTG 13027

RESULT 15
US-10-055-001A-24
; Sequence 24, Application US/10055001A
; Publication No. US20030049835A1
; GENERAL INFORMATION:
; APPLICANT: Wesley, Susan V.
; APPLICANT: Waterhouse, Peter
; APPLICANT: Helliwell, Christopher A.
; TITLE OF INVENTION: Method and means for producing efficient silencing constructs
; TITLE OF INVENTION: using recombinational cloning
; FILE REFERENCE: HELIGA
; CURRENT APPLICATION NUMBER: US/10/055,001A
; CURRENT FILING DATE: 2002-06-11
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 24
; LENGTH: 17476
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: acceptor vector pHELLSGATE8
US-10-055-001A-24

Query Match          94.1%; Score 152.4; DB 15; Length 17476;
Best Local Similarity 96.3%; Pred. No. 5.8e-23;
Matches 156; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
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Db      16536  TCGACTACAGGTCACTAATACCATCTAAGTAGTTGATTCATAGTGCAGTGCATATCTTGTG 16595
Qy      61  TTTTACAGTATTATGTAGTCTGTTTTTTATGCAGAAATCTAATTTAATATATTGATATTTA 120
Db      16596  TTTTACAGTATTATGTAGTCTGTTTTTTATGCAGAAATCTAATTTAATATATTGATATTTA 16655
Qy     121  TATCATTTTACGTTTCTCGTTCAGCTTTTATATACTAACTTG 162
Db     16656  TATCATTTTACGTTTCTCGTTCAGCTTTTATATACTAACTTG 16697
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Search completed: September 10, 2004, 00:14:08
Job time : 204.654 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: September 9, 2004, 15:48:15 ; Search time 1118.24 Seconds
(without alignments)
6279.120 Million cell updates/sec

Title: US-10-082-772B-4
Perfect score: 162
Sequence: 1 tctgttacaggctcactaata.....agotTTTTtatactaacttg 162

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0
Searched: 3470272 segs, 21671516995 residues
Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

- GenEmbl.*
1: gb_ba.*
2: gb_btg.*
3: gb_in.*
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6: gb_pat.*
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32: em_htg_other.*
33: em_htg_mus.*
34: em_htg_pln.*
35: em_htg_rod.*
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40: em_htgo_mus.*
41: em_htgo_other.*

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description
1	162	100.0	162	6	AX092115	AX092115 Sequence
2	162	100.0	172	7	LAMPRCB	M12459 Bacterioph
3	160.4	99.0	243	6	AX092113	AX092113 Sequence
4	160.4	99.0	361	7	LAMINTATT	M23841 Bacterioph
5	160.4	99.0	610	6	AX101000	AX101000 Sequence
6	160.4	99.0	1688	9	MACHSS	D85521 Macaca fasc
7	160.4	99.0	1763	6	BD225932	BD225932 Immediate
8	160.4	99.0	2758	3	PFAHRPC	M17028 P.falciparu
9	160.4	99.0	3485	12	AF178449	AF178449 Integrati
10	160.4	99.0	3485	12	AF178450	AF178450 Integrati
11	160.4	99.0	4105	12	AF271663	AF271663 Cloning v
12	160.4	99.0	4190	12	XXU13848	U13848 pExcell clo
13	160.4	99.0	4549	12	AF178452	AF178452 Integrati
14	160.4	99.0	4549	12	AF178453	AF178453 Integrati
15	160.4	99.0	5641	6	AX113748	AX113748 Sequence
16	160.4	99.0	5670	6	AX113749	AX113749 Sequence
17	160.4	99.0	5826	6	AX113746	AX113746 Sequence
18	160.4	99.0	6000	12	U66308	U66308 Expression
19	160.4	99.0	6043	6	AR399301	AR399301 Sequence
20	160.4	99.0	6043	6	AX370644	AX370644 Sequence
21	160.4	99.0	6071	6	AX113747	AX113747 Sequence
22	160.4	99.0	7176	12	AF178451	AF178451 Integrati
23	160.4	99.0	42529	12	CVU39284	U39284 Cloning vec
24	160.4	99.0	42530	12	CVU39285	U39285 Cloning vec
25	160.4	99.0	42531	12	CVU39286	U39286 Cloning vec
26	160.4	99.0	42704	12	CVU37692	U37692 Cloning vec
27	160.4	99.0	48502	7	LAMCG	J02459 Bacterioph
28	158.8	98.0	243	6	AX092116	AX092116 Sequence
29	150.8	93.1	4204	6	BD263378	BD263378 Compositi
30	150.8	93.1	4208	6	BD263379	BD263379 Compositi
31	150.8	93.1	4470	6	BD263377	BD263377 Compositi
32	150.8	93.1	4939	6	BD263381	BD263381 Compositi
33	150.8	93.1	5584	6	BD263402	BD263402 Compositi
34	150.8	93.1	18691	12	CV8311874	AJ311874 Cloning v
35	150.8	93.1	18691	12	CV8311874	AJ311874 Cloning v
36	150.6	93.0	233	6	BD263225	BD263225 Compositi
37	150.6	93.0	233	6	AX787499	AX787499 Sequence
38	149.2	92.1	4165	6	BD263380	BD263380 Compositi
39	149.2	92.1	4204	6	BD263378	BD263378 Compositi
40	149.2	92.1	4208	6	BD263379	BD263379 Compositi
41	149.2	92.1	4470	6	BD263377	BD263377 Compositi
42	149.2	92.1	4939	6	BD263381	BD263381 Compositi
43	149.2	92.1	5156	6	BD263382	BD263382 Compositi
44	149.2	92.1	5584	6	BD263402	BD263402 Compositi
45	149	92.0	233	6	BD263226	BD263226 Compositi

ALIGNMENTS

RESULT 1
AX092115
LOCUS AX092115 162 bp DNA linear PAT 21-MAR-2001
DEFINITION Sequence 4 from Patent WO0116345.
ACCESSION AX092115
VERSION AX092115.1 GI:13444358
KEYWORDS
SOURCE Escherichia coli
ORGANISM Escherichia coli
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Escherichia.
REFERENCE 1
AUTHORS Droege, P.
TITLE Sequence-specific dna recombination in eukaryotic cells
JOURNAL Patent: WO 0116345-A 4 08-MAR-2001;

Pred. No. is the number of results predicted by chance to have a

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LOCUS       AX092113                243 bp    DNA             linear     PAT 21-MAR-2001
DEFINITION   Sequence 2 from Patent WO0116345.
ACCESSION    AX092113
VERSION      AX092113.1   GI:13444356
KEYWORDS     .
SOURCE       Bacteriophage lambda
ORGANISM     Bacteriophage lambda
            Viruses; dsDNA viruses, no RNA stage; Caudovirales; Siphoviridae;
            Lambda-like viruses.
REFERENCE    1
AUTHORS      Droegge, P.
TITLE        Sequence-specific dna recombination in eukaryotic cells
JOURNAL      Patent: WO 0116345-A 2 08-MAR-2001;
            Droegge, Peter (DE)
FEATURES     Location/Qualifiers
            source
            1..243
            /organism="Bacteriophage lambda"
            /mol_type="unassigned DNA"
            /db_xref="taxon:10710"

ORIGIN
Query Match          99.0%;   Score 160.4;   DB 6;   Length 243;
Best Local Similarity 99.4%;   Pred. No. 1.3e-20;
Matches 161;   Conservative 0;   Mismatches 1;   Indels 0;   Gaps 0;

QY      1  TCTGTTACAGGTCACCTAATACCACTAAGTAGTTCGATTCATAGTCAGTCGCATATGTTGG 60
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DB      1  TCTGTTACAGGTCACCTAATACCACTAAGTAGTTCGATTCATAGTCAGTCGCATATGTTGG 60

QY      61  TTTTACAGTATTATGATGCTGTTTTTATGCAAAATCTAAATTTAATATATTGATATTTA 120
          |||||||
DB      61  TTTTACAGTATTATGATGCTGTTTTTATGCAAAATCTAAATTTAATATATTGATATTTA 120

QY      121  TATCATTTTACGTTTCTCGTTCAGCTTTTATATACTAACTTG 162
          |||||||
DB      121  TATCATTTTACGTTTCTCGTTCAGCTTTTATATACTAACTTG 162

RESULT 4
LAMINTATT/c
LOCUS       LAMINTATT                361 bp    DNA             linear     PHG 28-APR-1993
DEFINITION   Bacteriophage lambda int gene region.
ACCESSION    M23841
VERSION      M23841.1   GI:215177
KEYWORDS     site-specific recombination.
SOURCE       Bacteriophage lambda
ORGANISM     Bacteriophage lambda
            Viruses; dsDNA viruses, no RNA stage; Caudovirales; Siphoviridae;
            Lambda-like viruses.
REFERENCE    1 (bases 1 to 361)
AUTHORS      Schmeissner, U., McKenney, K., Rosenberg, M. and Court, D.
TITLE        Removal of a terminator structure by RNA processing regulates int
            gene expression
JOURNAL      J. Mol. Biol. 176 (1), 39-53 (1984)
MEDLINE      84242838
PUBMED       6234400
COMMENT      Original source text: Bacteriophage lambda DNA.
FEATURES     Location/Qualifiers
            source
            1..361
            /organism="Bacteriophage lambda"
            /mol_type="genomic DNA"
            /db_xref="taxon:10710"

ORIGIN
Query Match          99.0%;   Score 160.4;   DB 7;   Length 361;
Best Local Similarity 99.4%;   Pred. No. 1.2e-20;
Matches 161;   Conservative 0;   Mismatches 1;   Indels 0;   Gaps 0;

QY      1  TCTGTTACAGGTCACCTAATACCACTAAGTAGTTCGATTCATAGTCAGTCGCATATGTTGG 60
          |||||||
DB      259  TCTGTTACAGGTCACCTAATACCACTAAGTAGTTCGATTCATAGTCAGTCGCATATGTTGG 200

QY      61  TTTTACAGTATTATGATGCTGTTTTTATGCAAAATCTAAATTTAATATATTGATATTTA 120
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FEATURES     source
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            /organism="Bacteriophage lambda"
            /mol_type="genomic DNA"
            /db_xref="taxon:10710"

ORIGIN
Query Match          100.0%;   Score 162;   DB 7;   Length 172;
Best Local Similarity 100.0%;   Pred. No. 7.1e-21;
Matches 162;   Conservative 0;   Mismatches 0;   Indels 0;   Gaps 0;

QY      1  TCTGTTACAGGTCACCTAATACCACTAAGTAGTTCGATTCATAGTCAGTCGCATATGTTGG 60
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DB      11  TCTGTTACAGGTCACCTAATACCACTAAGTAGTTCGATTCATAGTCAGTCGCATATGTTGG 70

QY      61  TTTTACAGTATTATGATGCTGTTTTTATGCAAAATCTAAATTTAATATATTGATATTTA 120
          |||||||
DB      71  TTTTACAGTATTATGATGCTGTTTTTATGCAAAATCTAAATTTAATATATTGATATTTA 130

QY      121  TATCATTTTACGTTTCTCGTTCAGCTTTTATATACTAACTTG 162
          |||||||
DB      131  TATCATTTTACGTTTCTCGTTCAGCTTTTATATACTAACTTG 172

RESULT 3
AX092113
LAMPRCB
LOCUS       LAMPRCB                172 bp    DNA             linear     PHG 28-APR-1993
DEFINITION   Bacteriophage lambda site specific recombinant DNA (attr).
ACCESSION    M12459
VERSION      M12459.1   GI:215191
KEYWORDS     .
SOURCE       Bacteriophage lambda
ORGANISM     Bacteriophage lambda
            Viruses; dsDNA viruses, no RNA stage; Caudovirales; Siphoviridae;
            Lambda-like viruses.
REFERENCE    1 (bases 1 to 172)
AUTHORS      Bushman, W., Thompson, J.F., Vargas, L. and Landy, A.
TITLE        Control of directionality in lambda site specific recombination
JOURNAL      Science 230 (4728), 906-911 (1985)
MEDLINE      86044513
PUBMED       2932798
COMMENT      Original source text: Bacteriophage lambda DNA.
            Circular phage DNA (attP) and linear bacterial DNA (attB) undergo
            integrative recombinations to yield attL and attR. AttL and attR
            can undergo excisive recombination. Positions 159-165 demark the 7
            base pair overlap region.
FEATURES     Location/Qualifiers
            source
            1..172
            /organism="Bacteriophage lambda"
            /mol_type="genomic DNA"
            /db_xref="taxon:10710"

ORIGIN
Query Match          100.0%;   Score 162;   DB 7;   Length 172;
Best Local Similarity 100.0%;   Pred. No. 7.1e-21;
Matches 162;   Conservative 0;   Mismatches 0;   Indels 0;   Gaps 0;

QY      1  TCTGTTACAGGTCACCTAATACCACTAAGTAGTTCGATTCATAGTCAGTCGCATATGTTGG 60
          |||||||
DB      11  TCTGTTACAGGTCACCTAATACCACTAAGTAGTTCGATTCATAGTCAGTCGCATATGTTGG 70

QY      61  TTTTACAGTATTATGATGCTGTTTTTATGCAAAATCTAAATTTAATATATTGATATTTA 120
          |||||||
DB      71  TTTTACAGTATTATGATGCTGTTTTTATGCAAAATCTAAATTTAATATATTGATATTTA 130

QY      121  TATCATTTTACGTTTCTCGTTCAGCTTTTATATACTAACTTG 162
          |||||||
DB      131  TATCATTTTACGTTTCTCGTTCAGCTTTTATATACTAACTTG 172

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199 TTTTACAGTATTAGTAGTCTGTTTTTATGCAAAATCTAATTAATATATGATATTTA 140
|||||
121 TATCATTTTACGTTTCTCGTTCAGCTTTTATTAATACTTG 162
|||||
139 TATCATTTTACGTTTCTCGTTCAGCTTTTATTAATACTTG 98
|||||

RESULT 5
AX101000
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Nicotiana tabacum (common tobacco)
Nicotiana tabacum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
asterids; lamids; Solanales; Solanaceae; Nicotiana.
REFERENCE
1
AUTHORS
Meyer, P.L. and Zubko, E.L.
TITLE
Targeted gene removal
JOURNAL
Patent: WO 0121780-A 1 29-MAR-2001;
THE UNIVERSITY OF LEEDS (GB)
FEATURES
source
1..610
Location/Qualifiers
/mol_type="unassigned DNA"
/db_xref="taxon:4097"
ORIGIN
Query Match 99.0%; Score 160.4; DB 6; Length 610;
Best Local Similarity 99.4%; Pred. No. 1.1e-20;
Matches 161; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TCTGTTACAGGTCACCTAATACCATCTAAGTAGTGTGATGATGAGCTGCATATGTTGTG 60
|||||
Db 139 TCTGTTACAGGTCACCTAATACCATCTAAGTAGTGTGATGATGAGCTGCATATGTTGTG 198
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QY 61 TTTTACAGTATTATGATGCTGTTTTTATGCAAAATCTAATTAATATATGATATTTA 120
|||||
Db 199 TTTTACAGTATTATGATGCTGTTTTTATGCAAAATCTAATTAATATATGATATTTA 258
|||||

QY 121 TATCATTTTACGTTTCTCGTTCAGCTTTTATTAATACTTG 162
|||||
Db 259 TATCATTTTACGTTTCTCGTTCAGCTTTTATTAATACTTG 300
|||||

RESULT 6
MACHSS/c
LOCUS
DEFINITION
Macaca fascicularis mRNA for hydroxysteroid sulfotransferase
subunit, complete cds.
ACCESSION
D85521
VERSION
D85521.1 GI:1345405
KEYWORDS
hydroxysteroid sulfotransferase subunit.
SOURCE
Macaca fascicularis (crab-eating macaque)
ORGANISM
Macaca fascicularis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
Cercopitheciinae; Macaca.
REFERENCE
1 (bases 1 to 1668)
AUTHORS
Ogura, K., Satsukawa, M., Kato, K., Okuda, H. and Watabe, T.
TITLE
Molecular cloning of monkey liver hydroxysteroid sulfotransferase
Unpublished
JOURNAL
2 (bases 1 to 1668)
AUTHORS
Ogura, K.
TITLE
Direct Submission
JOURNAL
Submitted (23-MAY-1996) Kenichiro Ogura, Tokyo University of
Pharmacy and Life Science, Department of Drug Metabolism and
Molecular Toxicology; 1432-1 Horinouchi, Hachioji, Tokyo 192-0392,
Japan (E-mail:ogurak@ps.toyaku.ac.jp, Tel: +81-426-76-4518,

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Fax: +81-426-76-4517)
FEATURES
source
Location/Qualifiers
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/organism="Macaca fascicularis"
/mol_type="mRNA"
/db_xref="taxon:9541"
/clone="monHST-1"
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611..1468
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/protein_id="BAAI2823.1"
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QLPPKFFSKAKVIYLMRNPRDVFVSGYFVFNVSFVKPKSQVQVFEWPCQGNVIY
GSWFHIGHMMPMRKKNFLLSYBELKODTRTVEKI COFLGKTLPEBLNLKNS
SQSKMKNSMNSFLLSVDFVEKEAQLLRKGISDKNHLTVAAEAADKLFOEKMTD
LPRELFPWE"
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Query Match 99.0%; Score 160.4; DB 9; Length 1668;
Best Local Similarity 99.4%; Pred. No. 8.5e-21;
Matches 161; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Db 391 TCTGTTACAGGTCACCTAATACCATCTAAGTAGTGTGATGATGAGCTGCATATGTTGTG 332
|||||

QY 61 TTTTACAGTATTATGATGCTGTTTTTATGCAAAATCTAATTAATATATGATATTTA 120
|||||
Db 331 TTTTACAGTATTATGATGCTGTTTTTATGCAAAATCTAATTAATATATGATATTTA 272
|||||

QY 121 TATCATTTTACGTTTCTCGTTCAGCTTTTATTAATACTTG 162
|||||
Db 271 TATCATTTTACGTTTCTCGTTCAGCTTTTATTAATACTTG 230
|||||

RESULT 7
BD225932/c
LOCUS
DEFINITION
Immediate early gene and method for using the same.
ACCESSION
BD225932
VERSION
BD225932.1 GI:33035702
KEYWORDS
JP 2002512772-A/49.
Rattus norvegicus (Norway rat)
SOURCE
Rattus norvegicus
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.
REFERENCE
1 (bases 1 to 1763)
AUTHORS
Worley, P.F., Lanahan, A., Goetz, B., Hiemisch, H., Kuner, R.,
Scheek, S., Nikolich, K. and Zhukovski, E.
TITLE
Immediate early gene and method for using the same
JOURNAL
Patent: JP 2002512772-A 49 08-MAY-2002;
THE JOHNS HOPKINS UNIVERSITY SCHOOL OF MEDICINE, BASF LYNX
BIOSCIENCE AG
COMMENT
OS Rattus norvegicus (rat)
PN JP 2002512772-A/49
PD 08-MAY-2002
PF 05-FEB-1999 JP 2000530634
PI 09-FEB-1998 US 60/074135, 12-FEB-1998 US 60/074518
PAUL F WORLEY, ANTHONY LANAHAN, BERNARD GOETZ, HOLGER HIEMISCH, PI
ROHINI KUNER,
PI SIGRID SCHEEK, KAROLY NIKOLICH, EUGENE ZHUKOVSKI PC
C12N15/09, A61K31/711, A61K48/00, A61P25/00, A61P25/28, C07H21/04, PC
C07K14/47,
PC C07K16/18, C12N1/15, C12N1/19, C12N1/21, C12N5/10, C12P21/08 PC
C12Q1/68, G01N33/53,
PC C12N15/00, C12N5/00
CC n is either a, t, g, or c

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FH key Location/Qualifiers
FT misc feature (1). (1763).
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Best Local Similarity 99.4%; Pred. No. 8.4e-21;
Matches 161; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 TCTGTTACAGGTCACATATACCATCTAGTCTAGTCTGATTCATAGTCACTGTCATATCTTGTG 60
Db 431 TCTGTTACAGGTCACATATACCATCTAGTCTAGTCTGATTCATAGTCACTGTCATATCTTGTG 372
QY 61 TTTTACAGTATATAGTCTGCTTTTATGCAAAATCTAAATTAATATATGATATTTA 120
Db 371 TTTTACAGTATATAGTCTGCTTTTATGCAAAATCTAAATTAATATATGATATTTA 312
QY 121 TATCATTTTACGTTTCTGCTGCTTTTATATCACTT 162
Db 311 TATCATTTTACGTTTCTGCTGCTTTTATATCACTT 270

RESULT 8
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LOCUS P.falciiparum histidine-rich protein genes. linear INV 26-APR-1993
DEFINITION M17028
ACCESSION M17028
VERSION 1
KEYWORDS histidine-rich protein.
SOURCE Plasmodium falciiparum (malaria parasite P. falciiparum)
ORGANISM Eukaryota; Alveolata; Apicomplexa; Haemosporidia; Plasmodium.
REFERENCE 1 (bases 1 to 2758)
AUTHORS Lenstra,R., d'Auriol,L., Andrien,B., Le Bras,J. and Gallibert,F.
TITLE Cloning and sequencing of Plasmodium falciiparum DNA fragments
  containing repetitive regions potentially coding for histidine-rich
  proteins: identification of two overlapping reading frames
  Biochem. Biophys. Res. Commun. 146 (1), 368-377 (1987)
JOURNAL 3038111
MEDLINE 87270765
COMMENT source text: P.falciiparum, cDNA to mRNA, clone M4.
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Best Local Similarity 99.4%; Pred. No. 7.6e-21;
Matches 161; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 TCTGTTACAGTCTAATACATCACTAAGTAGTGTGATTCATAGTCACTGTCATATCTTGTG 60
Db 2548 TCTGTTACAGTCTAATACATCACTAAGTAGTGTGATTCATAGTCACTGTCATATCTTGTG 2489
QY 61 TTTTACAGTATATAGTCTGCTTTTATGCAAAATCTAAATTAATATATGATATTTA 120
Db 2488 TTTTACAGTATATAGTCTGCTTTTATGCAAAATCTAAATTAATATATGATATTTA 2429
QY 121 TATCATTTTACGTTTCTGCTGCTTTTATATCACTT 162
Db 2428 TATCATTTTACGTTTCTGCTGCTTTTATATCACTT 2387

RESULT 9
AF178449
LOCUS AF178449
DEFINITION Integration vector pCD11PKS chloramphenicol transacetylase (cat)
  and beta-galactosidase alpha peptide (lacZa) genes, complete cds.
ACCESSION AF178449
VERSION AF178449.1
KEYWORDS
  SOURCE
    Integration vector pCD11PKS
    Integration vector pCD11PKS
    artificial sequences; vectors.
  1 (bases 1 to 3485)
  Platt,R., Drescher,C., Park,S.K. and Phillips,G.J.
  Genetic system for reversible integration of DNA constructs and
  lacZ gene fusions into the Escherichia coli chromosome
  Plasmid 43 (1), 12-23 (2000)
  JOURNAL 20079288
  MEDLINE 10610816
  PUBMED
REFERENCE 2 (bases 1 to 3485)
AUTHORS Platt,R., Drescher,C., Park,S.K. and Phillips,G.J.
TITLE Direct Submission
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JOURNAL Submitted (18-AUG-1999) Microbiology, Iowa State University, 207
 Science I Building, Ames, IA 50011, USA

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 /lab_host="Escherichia coli"

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 1. .385
 /notes="R6Kgamma"

misc_feature
 668. .915
 /note="attP; attachment site from bacteriophage lambda"

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CDS
 complement (1327. .1986)
 /gene="cat"

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protein_id="AAF86671.1"
 /db_xref="GI:9294787"

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 SSLWSYHDDFROFLHYQDVACYGENLAYFPKGFENNFFVSNPWSFTSFDLNV
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complement (2754. .3137)
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complement (2754. .3137)
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protein_id="AAF86670.1"
 /db_xref="GI:9294786"

translation="MTMTIPSAQLTLTKGNKSWPGPGRSTVSIILNSQSPGDL
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misc_feature
 2972. .3081
 /note="multiple cloning site"

ORIGIN
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 Best Local Similarity 99.4%; Pred. No. 7.2e-21;
 Matches 161; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TCTGTTACAGGTCACCTAATACCATCTAAGTAGTTGATTCATAGTCACTGCATGATGTTGTG 60
 Db TCTGTTACAGGTCACCTAATACCATCTAAGTAGTTGATTCATAGTCACTGCATGATGTTGTG 732

QY 61 TTTTACAGTATTATGAGTCTGTTTTTATGCAAAATCTAATTAATATATGATATTTA 120
 Db TTTTACAGTATTATGAGTCTGTTTTTATGCAAAATCTAATTAATATATGATATTTA 792

QY 121 TATCATTTTACGTTCTCGTTACGCTTTTATGCAAAATCTAATTAATATGATATTTA 162
 Db TATCATTTTACGTTCTCGTTACGCTTTTATGCAAAATCTAATTAATATGATATTTA 834

RESULT 10
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 LOCUS 3485 bp DNA linear SYN 20-JUL-2000
 DEFINITION Integration vector pCD11PSK chloramphenicol transacetylase (cat)
 and beta-galactosidase alpha peptide (lacZa) genes, complete cds.
 ACCESSION AFI78450
 VERSION AFI78450.1 GI:9294788
 KEYWORDS integration vector pCD11PSK
 SOURCE Integration vector pCD11PSK
 ORGANISM artificial sequences; vectors.
 REFERENCE 1 (bases 1 to 3485)
 AUTHORS Platt, R., Drescher, C., Park, S.K. and Phillips, G.J.
 TITLE Genetic system for reversible integration of DNA constructs and

lacZ gene fusions into the Escherichia coli chromosome

Plasmid 43 (1), 12-23 (2000)

20079288
 10610816

REFERENCE 2 (bases 1 to 3485)
 AUTHORS Platt, R., Drescher, C., Park, S.K. and Phillips, G.J.
 TITLE Direct Submission
 JOURNAL Submitted (18-AUG-1999) Microbiology, Iowa State University, 207
 Science I Building, Ames, IA 50011, USA

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 /organism="Integration vector pCD11PSK"
 /mol_type="genomic DNA"
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misc_feature
 668. .915
 /note="attP; attachment site from bacteriophage lambda"

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CDS
 complement (1327. .1986)
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protein_id="AAF86673.1"
 /db_xref="GI:9294790"

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 SSLWSYHDDFROFLHYQDVACYGENLAYFPKGFENNFFVSNPWSFTSFDLNV
 ANMNFPAFVFTMGKYITQGDVKVLMPLAIQVHHAUCDGHVGRMLNELQQYCDWQGG
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complement (2754. .3137)
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complement (2754. .3137)
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 /product="beta-galactosidase alpha peptide"

protein_id="AAF86672.1"
 /db_xref="GI:9294789"

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ORIGIN
 Query Match 99.0%; Score 160.4; DB 12; Length 3485;
 Best Local Similarity 99.4%; Pred. No. 7.2e-21;
 Matches 161; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TCTGTTACAGGTCACCTAATACCATCTAAGTAGTTGATTCATAGTCACTGCATGATGTTGTG 60
 Db TCTGTTACAGGTCACCTAATACCATCTAAGTAGTTGATTCATAGTCACTGCATGATGTTGTG 732

QY 61 TTTTACAGTATTATGAGTCTGTTTTTATGCAAAATCTAATTAATATGATATTTA 120
 Db TTTTACAGTATTATGAGTCTGTTTTTATGCAAAATCTAATTAATATGATATTTA 792

QY 121 TATCATTTTACGTTCTCGTTACGCTTTTATGCAAAATCTAATTAATATGATATTTA 162
 Db TATCATTTTACGTTCTCGTTACGCTTTTATGCAAAATCTAATTAATATGATATTTA 834

RESULT 11
 AFI78450
 LOCUS 4105 bp DNA circular SYN 11-JUL-2000
 DEFINITION Cloning vector pLDR9, complete sequence.
 ACCESSION AFI78450
 VERSION AFI78450.1 GI:9022390
 KEYWORDS

SOURCE	Cloning vector pLDR9		
ORGANISM	Cloning vector pLDR9		
REFERENCE	1 (bases 1 to 4105)		
AUTHORS	Wiencis,A.M., Keagle,P., Andersen,J., Wotanis,J., Newcombe,R. and August,P.R.		
TITLE	Direct Submission		
JOURNAL	Submitted (24-MAY-2000) Molecular Genomics, Aventis Pharmaceuticals, 26 Landsdowne Street, Cambridge, MA 02139, USA		
FEATURES	Location/Qualifiers		
source	1..4105		
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	216..1031		
	/function="confers kanamycin resistance"		
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CDS	1528..2388		
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	/note="derived from pMMB66EH"		
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	/transl_table=11		
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	/db_xref="GI:9022391"		
	/translation="MSIQHPRVALIPFFAAFCLPVFAHPETLVKVKDAEDQLGARVY IEIDLNSKILSEFRPEERPMSTFKVLICGAVLRVDAQOLGRRIRHYSQNDLVE YSYVTEKHLIDVRELCTSCAAITMDSNTAANLLTTIGPKELTAFLENMGDHVTRL DRWPELNEAIPNDRITMTVPAMATTLRKLTIGELLTLASRQQLIDMWAEADKVAQPL LRGALPAGWFIADKSGAGERSGIIAALPGDKPSKRVIVITYTTSQATMDERNRQIA EIGASLIKKW"		
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Qy	1	TCGTGTACAGGTCACCTAATACCACTCTAAGTAGTGTGATTCATAGTGA	CTGCATATGTTGTG 60
Db	2617	TCGTGTACAGGTCACCTAATACCACTCTAAGTAGTGTGATTCATAGTGA	CTGCATATGTTGTG 2676
Qy	61	TTTTACAGTATTATGAGTCTGTTTTTATGCAAAATCTAAATTAATATTCATATTA	120
Db	2677	TTTTACAGTATTATGAGTCTGTTTTTATGCAAAATCTAAATTAATATTCATATTA	2736
Qy	121	TATCAATTTTACGTTTCTCGTTACGTTCTTTTATACAACTTG	162
Db	2737	TATCAATTTTACGTTTCTCGTTACGTTCTTTTATACAACTTG	2778
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XXU13848/c			
LOCUS	XXU13848	4190 bp	DNA circular SYN 13-DEC-1994


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production of single-stranded DNA; base 2933 represents
the first base of the newly synthesized single strand"
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Best Local Similarity 99.4%; Pred. No. 6.9e-21;
Matches 161; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 TCTGTTACAGGTCACCTAATACCACTCTAAGTAGTTGATTCATAGTACGCTGCATATGTTGTG 60
Db 4089 TCTGTTACAGGTCACCTAATACCACTCTAAGTAGTTGATTCATAGTACGCTGCATATGTTGTG 4030
QY 61 TTTTACAGTATTATAGTCTGTTTTTTATGCAAAATCTAATTAATATATGATATTTA 120
Db 4029 TTTTACAGTATTATAGTCTGTTTTTTATGCAAAATCTAATTAATATATGATATTTA 3970
QY 121 TATCATTTTACGTTCTCGTTCAGCTTTTATTAATACTAAGTTG 162
Db 3969 TATCATTTTACGTTCTCGTTCAGCTTTTATTAATACTAAGTTG 3928
RESULT 13
AF178452
LOCUS 4549 bp DNA linear SYN 20-JUL-2000
DEFINITION Integration vector pCD13PKS aminoglycoside adenylyltransferase (aadA)
and beta-galactosidase alpha peptide (lacZa) genes, complete cds.
ACCESSION AF178452
VERSION AF178452.1 GI:9294794
KEYWORDS
SOURCE Integration vector pCD13PKS
ORGANISM Integration vector pCD13PKS
artificial sequences; vectors.
REFERENCE 1 (bases 1 to 4549)
AUTHORS Platt,R., Drescher,C., Park,S.K. and Phillips,G.J.
TITLE Genetic system for reversible integration of DNA constructs and
lacZ gene fusions into the Escherichia coli chromosome
JOURNAL Plasmid 43 (1), 12-23 (2000)
MEDLINE 20079288
PUBMED 10610816
REFERENCE 2 (bases 1 to 4549)
AUTHORS Platt,R., Drescher,C., Park,S.K. and Phillips,G.J.
TITLE Direct Submission
JOURNAL Submitted (18-AUG-1999) Microbiology, Iowa State University, 207
Science I Building, Ames, IA 50011, USA
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668..915
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EHSVALVPAAEELFDVPEQDLFEALNETLTLWNSPPDWAGDNRNVLTLSRIWYSA
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Best Local Similarity 99.4%; Pred. No. 6.8e-21;
Matches 161; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 TCTGTTACAGGTCACCTAATACCACTCTAAGTAGTTGATTCATAGTACGCTGCATATGTTGTG 60
Db 673 TCTGTTACAGGTCACCTAATACCACTCTAAGTAGTTGATTCATAGTACGCTGCATATGTTGTG 732
QY 61 TTTTACAGTATTATAGTCTGTTTTTTATGCAAAATCTAATTAATATATGATATTTA 120
Db 733 TTTTACAGTATTATAGTCTGTTTTTTATGCAAAATCTAATTAATATATGATATTTA 792
QY 121 TATCATTTTACGTTCTCGTTCAGCTTTTATTAATACTAAGTTG 162
Db 793 TATCATTTTACGTTCTCGTTCAGCTTTTATTAATACTAAGTTG 834
RESULT 14
AF178453
LOCUS 4549 bp DNA linear SYN 20-JUL-2000
DEFINITION Integration vector pCD13PKS aminoglycoside adenylyltransferase (aadA)
and beta-galactosidase alpha peptide (lacZa) genes, complete cds.
ACCESSION AF178453
VERSION AF178453.1 GI:9294797
KEYWORDS
SOURCE Integration vector pCD13PKS
ORGANISM Integration vector pCD13PKS
artificial sequences; vectors.
REFERENCE 1 (bases 1 to 4549)
AUTHORS Platt,R., Drescher,C., Park,S.K. and Phillips,G.J.
TITLE Genetic system for reversible integration of DNA constructs and
lacZ gene fusions into the Escherichia coli chromosome
JOURNAL Plasmid 43 (1), 12-23 (2000)
MEDLINE 20079288
PUBMED 10610816
REFERENCE 2 (bases 1 to 4549)
AUTHORS Platt,R., Drescher,C., Park,S.K. and Phillips,G.J.
TITLE Direct Submission
JOURNAL Submitted (18-AUG-1999) Microbiology, Iowa State University, 207
Science I Building, Ames, IA 50011, USA
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/organism="Integration vector pCD13PKS"
/mol_type="genomic DNA"
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/notes="R6Kgamma"
668..915
/notes="attP; attachment site from bacteriophage lambda"
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complement(1798..2652)
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/protein_id="AAF86673.1"
/db_xref="GI:9294799"
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EHSVALVGPAAEELFDPPVEODLPEALNETLTKNSPPDWAGDERNVLTLSRIWYSA
VTGKTAPKDVAADWAMERLPAQYQPVILEARQAYLGQEDRLASRADQLERFVHVVK
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/translation="WTMTTPSAQLTLTKGNKSWSTAVAAALELVDPGCRNSISLS
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misc_feature 4038..4145
/note="multiple cloning site"

ORIGIN

Query Match 99.0%; Score 160.4; DB 12; Length 4549;
Best Local Similarity 99.4%; Pred. No. 6.8e-21; Mismatches 1; Indels 0; Gaps 0;
Matches 161; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 TCTGTTACAGGTCACATAACCATCTAAGTAGTTGATTCATAGTCGATGTCATATGTTGTG 60
Db TCTGTTACAGGTCACATAACCATCTAAGTAGTTGATTCATAGTCGATGTCATATGTTGTG 732
QY 61 TTTTACAGTATTATGTCGTCTGTTTTTATGCAAAATCTAAATTTAATATGATATTTA 120
Db TTTTACAGTATTATGTCGTCTGTTTTTATGCAAAATCTAAATTTAATATGATATTTA 792
QY 121 TATCATTTTACGTTTCTCGTTCAGCTTTTATATACTAACTTG 162
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RESULT 15
AX113748
LOCUS AX113748 5641 bp DNA linear PAT 01-MAY-2001
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AUTHORS Zyskind, J.
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Elitra Pharmaceuticals, Inc. (US)
FEATURES
source
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/note="pJMF3"

ORIGIN

Query Match 99.0%; Score 160.4; DB 6; Length 5641;
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Db TCTGTTACAGGTCACATAACCATCTAAGTAGTTGATTCATAGTCGATGTCATATGTTGTG 4762
QY 61 TTTTACAGTATTATGTCGTCTGTTTTTATGCAAAATCTAAATTTAATATGATATTTA 120
Db TTTTACAGTATTATGTCGTCTGTTTTTATGCAAAATCTAAATTTAATATGATATTTA 4822
QY 121 TATCATTTTACGTTTCTCGTTCAGCTTTTATATACTAACTTG 162
Db TATCATTTTACGTTTCTCGTTCAGCTTTTATATACTAACTTG 4864
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